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Database
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Listing first 45 summaries
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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
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geneseqp2001s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	ທ	4.	ω	N	ب	Result No.	
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	Art	M -	Abb84108 GUS prote		Aaw93824 Human GUS		Fugi	Prot	Rat Prot		Aae02444 Murine be			Aam48998 L gasseri		æ	Aaw93821 Bacillus	N	Aaw93826 Bacillus	Aaw93822 Bacillus	σ	Aaw93820 Bacillus		σ.	Description	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	
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28.8	28.8	28.8	28.8	28.8	28.8	28.8	29.0	29.0	29.1	29.1	29.1	29.1	29.1	29.2	29.2	29.2	29.2	29.2	
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Add45481	Aae02443	Aab62271	Aab62276	Aab28407	Aaw93828	Aaw93823	Aap82948	Aaw04302	Abb84637	Abb81108	Abr83626	Ads26258	Aaw42429	Add27991	Add27989	Add27986	Abb84107	Aar43387	
Human Pro	Human bet	Heavy cha	Mutant he	Escherich	Human GUS	E. coli G	Beta-gluc	Antibody/	LUC-U3'-U	LUC-U3'-U	SUMO-beta	Bacterial	Escherich	Caleosin/	Oleosin/b	Beta-gluc	GUS prote	Beta-gluc	

ALIGNMENTS

RESULT 1 AAB28406 Microbial; beta-glucoronidase; GUS; Enterobacter; Salmonella; Pseudomonas; Staphylococcus; Thermotoga; transgenic plant; bioindicator; AAB28406 standard; 21-SEP-2000. WO200055333-A1 Thermotoga maritima. transgenic insect; marker; glucuronide detoxification. Thermotoga maritima beta-glucoronidase. 26-JAN-2001 (first entry) AAB28406; protein; 563 ጅ

17-MAR-1999; 16-MAR-2000; 2000WO-US007107.

WPI; 2000-647075/62. N-PSDB; AAA07937. Jefferson RA, Mayer JE;

(CAMB-) CAMBIA BIOSYSTEMS LLC

99US-00270957.

Novel microbial beta-glucuronidase genes and gene products used as reporter/effector molecule, as diagnostic tool, in positive selection, to target molecules to specific cells and to detect and track linked genes.

Claim 3; Fig 5B; 116pp; English.

The present sequence is a microbial beta-glucuronidase (GUS) protein. GUS genes were obtained from six different genera: Enterobacter/Salmonella, Pseudomonas, Salmonella, Staphylococcus and Thermotoga. Microbial GUS can be used as a reporter/effector molecule for transgenic constructions and in in vitro diagnostic applications. It may also be used to generate sentinel plants that serve as bioindicators of environmental status. It may be used to generate transgenic insects for tracking insect populations or to facilitate the development of a bioassay for compounds that affect molecules critical for insect development (e.g. juvenile hormone). Secreted GUS may also serve as a marker for beneficial fungi destined . Secreted GUS may also serve as a marker for benefic: for release into the environment. In animal systems,

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Best Local S
Matches 563
                       Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; pathogen tolerance; plant growth regulator; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;
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                                                                                                                                                                                                    Bacterial
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     nitrogen; phosphorus;
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Query Match Best Local : Matches 56

Similarity

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The invention relates to a recombinant DNA construct comprising a CC provide for expression of a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a CC microbial source. The invention also relates to a transformed plant CC comprising the recombinant DNA construct and a method of producing a CC transformed plant having an improved property. The plant is a crop-plant CC such as maize or soybean. The method of producing a transformed plant with the recombinant DNA construct and growing the transformed plant with the complication of the plant properties and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plant, where the improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by production. This sequence represents a bacterial polypeptide used in the growth part of the printed specification or improved galactomannan of conduction. Note: The sequence data for this patent did not format from USPTO at sequence data for this patent did not format from USPTO at sequence data for this patent did not format from USPTO at sequence data for this patent did not format from USPTO at sequence data for this patent did not format from USPTO at sequence data for this patent did not format from USPTO at sequence data for this patent did not format from USPTO at sequence data for this patent did not format from USPTO at sequence data for this patent did not format from USPTO at sequence data for this patent did n
New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
Sequence
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                                                                                                                                   This invention describes a novel secreted form of Bacillus sp. beta-glucuronidase (BoGUS). The microbial BoGUS polypeptide can be used as reporter/effector molecule and as al dagnostic tool. The products of tinvention can be used as markers for transgene constructions, e.g. in plants or insects. They can also be used for the cleavage and detoxification of glucuronides and to examine conjugation patterns of
                                                                        Sequence
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                                                                                                                                                                                                                                                                                                               Claim
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                                                                                                                                                                                                                                                                                                                   GUS; BoGUS; beta-glucuronidase; secreted; reporter molecule; receptor molecule; diagnostic tool; transgene construction; prinsect; cleavage; detoxification; glucuronide.
                                                                          09-SEP-1997;
                                                                                                                          09-SEP-1998;
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CAMB-) CAMBIA

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RESULT 5
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Best Local S
Matches 221
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                                    AAW93822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 602
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Pred. No. 5.1e-67;
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glucuronidase (BoGUS). The microbial BoGUS polypeptide can be used as
reporter/effector molecule and as a diagnostic tool. The products of
invention can be used as markers for transgene constructions, e.g. ir
plants or insects. They can also be used for the cleavage and
detoxification of glucuronides and to examine conjugation patterns of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GUS; BoGUS; beta-glucuronidase; secreted; reporter molecule; marker; receptor molecule; diagnostic tool; transgene construction; plant; insect; cleavage; detoxification; glucuronide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 5; 76pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-229241/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            602
HKNHPSVIMMSVANEPESNHPDAEGFFKALYETANEMD-RTRPVVMVSMMDAPDERTRDV
                                                                          LADRLGILVIDEAPHVGITRYHYN---
                                                                                                                                       RLYLNGKPVFLKGFGKHEEFPVLGQGTFYPLMIKDFNLLKWINANSFRTSHYPYSEEWLD
                                                                                                                                                                                   GKVVASTEGLSGNVEIPNVILWEPLNTYLYQIKVELVNDGLTIDVYBEPFGVRTVEVNDG
                                                                                                                                                                                                                                                                                                                                                                                                                        YEEGPFTYKTTFYVPKXLSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEVDVTGK 104
                                                                                                                    KFLINNKPFYFKGFGKHEDTPINGRGFNEASNVMDFNILKWIGANSFRTAHYPYSEELMR
                                                                                                                                                                                                                                                       GLHRPVKIYTTPFTYVEDISVVTDFNGP---TGTVTYTVDFQ----GKAETVKVSVVDEB
                                                                                                                                                                                                                                                                                      GIIRPVLIEFTDHARILDIWVDTSESEPEKKLGKVKVKIEVSEEAVGQEMTIKLG--EEE
                                                                                                                                                                                                                                                                                                                       LRDGMNRVTVAVDNIL
                                                                                                                                                                                                                                                                                                                                                        VKSGENELRVVVENRLKVGGFPSKVPDSGTHTVGFFGS-----FPPANFDFFPYG
                                                  LADREGIVVIDETPAVGV---HINFMATTGLGEGSERVSTWEKIRTFEHHQDVLREIVSR
                                                                                                                                                                                                                    KKIRTSNRFVEGEFILENARFWSLEDPYLYPLKVELEKDEYTLDI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MLYPINTETRGVFDLNGVWNFKLDYGKGLEEKWYESKLTDTISMAVPSSYNDIGVTKEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         microbial beta-glucuronidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kilian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIOSYSTEMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 929; DB 2;
Pred. No. 5.1e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                       DDSTLPVGLYSERHEEGLGKVIRNKPNFDFFNYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 602;
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                                                                                                                                                                                                                    -GIRTISWDEK
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                                                                                   EDNIRRMIDE
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RESULT 6
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XX Baci
XX GUS;
KW TRCE
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XX W 199-5
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Best Local Similarity
Matches 221; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel secreted form of Bacillus sp. beta-glucuronidase (BoGUS). The microbial BoGUS polypeptide can be used as reporter/effector molecule and as a diagnostic tool. The products of tinvention can be used as markers for transgene constructions, e.g. in plants or insects. They can also be used for the cleavage and detoxisization of glucuronides and to examine conjugation patterns of
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated microbial beta-glucuronidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-1999
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                                 VKSGENELRVVVENRLKVGGFPSKVPDSGTHTVGFFGS-----FPPANFDFFPYG 154
                                                                                                                                                                                                                                                                     MVRPQRNKKRFILILNGVWNLEV------TSKDRPIAVPGSWNE--QYQDLC
                                                                                            NHIGYVWYEREFTVPAYLKDQRIVLRFGSATHKAIVYVNGELVVEHKGGFLPFEAEINNS
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                                                                                                                                                YEEGPFTYKTTFYVPKXLSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEVDVTGK 104
                                                                                                                                                                                                           MLYPINTETRGVFDLNGVWNFKLDYGKGLEEKWYESKLTDTISMAVPSSYNDIGVTKEIR
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                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kilian A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIOSYSTEMS LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0058263P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76pp; English
                                                                                                                                                                                                                                                                                                                                                              31.0%; Score 929; DB 2; 35.6%; Pred. No. 5.1e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Keese
                                                                                                                                                                                                                                                                                                                            93; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       602
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                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                           Novel microbial beta-glucuronidase genes and gene products used as reporter/effector molecule, as diagnostic tool, in positive selection, target molecules to specific cells and to detect and track linked gene
The present sequence
                                                             Example 3;
                                                                                                                                                                                                                                         N-PSDB; AAA07930.
                                                                                                                                                                                                                                                                                                                            Jefferson RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microbial; beta-glucoronidase; GUS; Enterobacter; Salmonella; Pseudomonas; Staphylococcus; Thermotoga; transgenic plant; bitransgenic insect; marker; glucuronide detoxification.
                                                                                                                                                                                                                                                                     WPI; 2000-647075/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus beta-glucoronidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB28402;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAR-2000; 2000WO-US007107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200055333-A1
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                                                       Fig 3;
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                                                       116pp;
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   is a microbial
                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                          717
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beta-glucuronidase (GUS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes were obtained from six different genera: Enterobacter/Salmonella, Pseudomonas, Salmonella, Staphylococcus and Thermotoga. Microbial GUS can be used as a reporter/effector molecule for transgenic constructions and in in vitro diagnostic applications. It may also be used to generate sentinel plants that serve as bioindicators of environmental status. It may be used to generate transgenic insects for tracking insect populations or to facilitate the development of a bioassay for compounds that affect molecules critical for insect development (e.g. juvenile hormone). Secreted GUS may also serve as a marker for beneficial fungi
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                                                                                                                            TRDRKPKLAAHVFRERWTNI 595
                                                                                                                                                                                     TRDROPKLVAHVLRRLWSEV
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glucuronidase (BoGUS). The microbial BoGUS polypeptide can be used as
reporter/effector molecule and as a diagnostic tool. The products of t
invention can be used as markers for transgene constructions, e.g. in
plants or insects. They can also be used for the cleavage and
detoxification of glucuronides and to examine conjugation patterns of
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 618 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated microbial beta-glucuronidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jefferson RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GUS; BoGUS; beta-glucuronidase; secreted; reporter molecule; marker; receptor molecule; diagnostic tool; transgene construction; plant; insect; cleavage; detoxification; glucuronide.
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                                                                                                                                                                                                                                                 105 VKSGENELRVVVENRLKVGGFPSKVPDSGTHTVGFFGS-----FPPANFDFFPYG
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                                                                                                                                                                                                                                                                                                                                                                1 MVRPQRNKKRFILILNGVWNLEV------TSKDRPIAVPGSWNE--QYQDLC 44
LADRLGILVIDEAPHVGITRYHYN---
                                                                                                                                                                                                                                                                                                         YEEGPFTYKTTFYVPKXLSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEVDVTGK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig 4A-C; 76pp; English.
                                             KFLINNKPFYFKGFGKHEDTPINGRGFNEASNVMDFNILKWIGANSFRTAHYPYSEELMR
                                                               RLYLNGKPVFLKGFGKHEEFPVLGQGTFYPLMIKDFNLLKWINANSFRTSHYPYSEEWLD
                                                                                                   GKVVASTEGLSGNVEIPNVILWEPLNTYLYOIKVELVNDGLTIDVYEEPFGVRTVEVNDG
                                                                                                                                                            GLHRPVKIYTTPFTYVEDISVVTDFNGP---TGTVTYTVDFQ----GKAETVKVSVVDEE
                                                                                                                                                                                        GIIRPVLIEFTDHARILDIWVDTSESEPEKKLGKVKVKIEVSEEAVGQEMTIKLG--EEE
                                                                                                                                                                                                                     LRDGMNRVTVAVDNIL------DDSTLPVGLYSERHEEGLGKVIRNKPNFDFFNYA
                                                                                                                                                                                                                                                                              NHIGYVWYEREFTVPAYLKDORIVLRFGSATHKAIVYVNGELVVEHKGGFLPFEAEINNS
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                                                                                                                               KKIRTSNRFVEGEFILENARFWSLEDPYLYPLKVELEKDEYTLDI-----GIRTISWDEK
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                                                                                                                                                                                                                                                                                                                                                                                             93; Mismatches
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Pred. No. 5.2e-67;
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 -PETQKIA----EDNIRRMIDR
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The present sequence is a microbial beta-glucuronidase (GUS) protein. GUS CG genes were obtained from six different genera: Enterobacter/Salmonella, Estabhylococcus and Thermotoga. Microbial GUS can CC be used as a reporter/effector molecule for transgenic constructions and CC in in vitro diagnostic applications. It may also be used to generate transgenic insects of environmental status. It CC may be used to generate transgenic insects for tracking insect compounds that affect molecules critical for insect development (e.g. juvenile CC that affect molecules critical for insect development (e.g. juvenile CC thornone). Secreted GUS may also serve as a marker for beneficial fungi CC Gustined for release into the environment. In animal systems, secreted GUS may be used to achieve extracellular detoxification of glucuronides (e.g. toxin glucuronide) and to examine conjugation patterns of glucuronides. Microbial GUS may also be used in traditional medical CC diagnostic assays, for drug testing, pharmacokinetic studies, following the status of diagnostic assays, for drug testing, pharmacokinetic studies.
diagnostic assays, for drug testing, pharmacokinetic studies, bicavailability studies, diagnosis of diseases and syndromes, progression of disease or its response to therapy. Microbial (
                                                                                                                                                                                                                                                                                                                                                                                  Novel microbial beta-glucuronidase genes and gene products used as reporter/effector molecule, as diagnostic tool, in positive selection, target molecules to specific cells and to detect and track linked gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Microbial; beta-glucoronidase; GUS; Enterobacter; Salmonella; Pseudomonas; Staphylococcus; Thermotoga; transgenic plant; bioindicator; transgenic insect; marker; glucuronide detoxification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jefferson
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DB; AAA07938.
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Best Local
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584
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RKPKLAAHVFRERWINI
                            ROPKLVAHVLRRLWSEV
                                                          DIDPVMFTEEYQVEYYQANHVVFDEFENFVGEQAWNFADFATSQGVMRVQGNKKGVFTRD
                                                                                      YDPPQMFSEEYQAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVFTRD
                                                                                                                                                YFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHR----KPIFVTEFGADAIAGIH
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                                                                                                                    LIDVIALNRYNGWYFDGGDLEAAKVHLR----QEFHAWNKRCPGKPIMITEYGADTVAGFH
                                                                                                                                                                               HPSVVMWSIANEAATEEEGAYEYFKPLVELTKELDPQKRPVTIVLFVMATPE--TDKVAE
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Pred.
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                                                                                                                                                                                                                                                                       ---PETQKIA----EDNIRRMIDRHKN
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RESULT 10
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AC AAB28
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DT 26-JA
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KW Pseud
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                                                                Microbial; beta-glucoronidase; GUS; Enterobacter; Salmonella; Pseudomonas; Staphylococcus; Thermotoga; transgenic plant; bi transgenic insect; marker; glucuronide detoxification.
                                                                                                                          Salmonella
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                                                                                                                                                                                                             AAB28409
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                                                                                                                          beta-glucoronidase
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bioindicator;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                  DEAPHVGI -----
                                                                                                                                LKGFGKHEEFPVLGQGTFYPLMIKDFNLLKWINANSFRTSHYPYSEEWLDLADRLGILVI
                                                                                                                                                                                                                        VEGEFILENARFWSLEDPYLYPLKV----ELEKDEYTLDIGIRTISWDEKRLYLNGKPVF
                                                                                                                                                                                                                                                                                         LYTTPKTFVEDITVVTQVAD----DLAQATVAWQVRANG----EVRVELRDAEQQLVASGQG
                                                                                                                                                                                                                                                                                                                                                                                         LISAGESVRITVCVNNELNWQTIP-----PGVVTQGVNGKKQQAYFHDFFNYAGIHRSVM
                                                                                                                                                                                                                                                                                                                                                                                                                                         KVKSGEN-ELRVVVENRLKVGGFPSKVPDSGTHTVGFFGSFPPANF-DFFPYGGIIRPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNYVGNVWYQREIRIPKGWDRQRIVLRFDAVTHYGKVWVNDQFLMEHQGGYTPFEADISH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYEEGPFTYKTTFYVPKXLSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEVDVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MVRPQRNKKRFILILNGVWNLEVTSKD------RPIAVPGSWNEQY--QDL
                                                                                               FTGFGRHEDADLRGKGFDNVLMVHDHALMDWIGANSYRTSHYPYAEEMLDWADEHGIVII
                                                                                                                                                                                               EKGELLLEGPRLWQPGEGYLYELRVIAQHQDEQDEYPLRVGIRSVEVKGEQFLINHKPFY
                                                                                                                                                                                                                                                                                                                                         IEFTDHARILDIWYDTSESEPEKKLGKVKVKIEVSEEAVGQEMTIKLGEEEKKIRTSNRF
DETAAVGFNLSLGISFDVGEKPKELYSDEAVNDETORAHLOAIKELIARDKNHPSVVMWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MLRSVETATREIKKLDGLWSFCMDSEECGNAQQWWRQPLPQSRAIAVPGSYNDQFAAAEI
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35.3%;
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                                             -----TRYHYNPETQKIAEDNIRRMIDRHKNHPSVIMWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 920; DB 3; Pred. No. 2.8e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 602;
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RESULT 11
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                                                                                                                                Matches
                                                                                                                                                        Query Match
                                                                                                                                                                                                        The present invention provides the protein and coding sequences Lactobacillus gasseri beta-glucuronidase (GUS). The protein has activity at acidic pHs, and thus can be used to detect low pH environments. The present sequence is the protein of the inventi
                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid of Lactobacillus gasseri encoding beta glucuronidase having activity at acidic pH which is useful as reporter protein for highly aciduric organisms, or as marker of transformed celi
                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                          Claim 19; Page 49-51; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              Russell WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beta-glucuronidase; GUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L gasseri beta-glucuronidase
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                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAL44836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM48998 standard; protein; 598
                                                                                                                                                                                                                                                                                                                                                                                                                        (UYNC-) UNIV
                                                                                                                                            Local
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                                                                                                                              207;
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108 GE-NELRVVVENRLKVGGFP---SKVPDSGTHTVGFFGSFPPANFDFFPYGGIIRPVLIE 163
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                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVFTRDRQPKLVAHVLR
                         GDFWYQKDFFIPSFLKKKELYIRFGSVTHRAKVFINGHEVGQHEGGFLPFQVKISNYINY
                                                 GPFTYKTTFYVPKXLSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEVDVTGKVKS
                                                                                                     PQRNKKRFILILNGVWNLEVT-----SKDRP----IAVPGSWNE--QYQDLCYEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IANEPDTRPNGAREYFAPLAQATRELDPTRPITCVNVMFCDAESDTITDL----FDVVCL
                                                                            PIQNKYRFNTLMNGTWQFETDPNSVGLDEGWNKELPDPEEMPVPGTFABLTTKRDRKYYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NRYYGWYVQSGDLEKAEKVLEKELLAWQEKLHRPIIITEYGVDTLAGLHSMYNDMWSEEY
                                                                                                                                Conservative
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34.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              low pH; Lactobacillus.
                                                                                                                              110;
                                                                                                                                            Score 919.5; DE Pred. No. 3e-66;
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                                                                                                                                Mismatches
                                                                                                                                                        DB 5;
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RESULT 12
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XX ADQ89
XX ADQ89
XX Cytos
XX Cytos
XX Cytos
XX Cell
XX Cytos
XX Cell
XX Cell
XX Incas
PN W0200
XX 31-DE
XX Incas
PR 10-JA
PR N-PSC
XX WPI;
DR N-PSC
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  Claim
                                     New cell cycle progression genes and proteins for modulating cell progression in cells, for preventing, treating or diagnosing cell proliferative diseases (e.g. cancer) or for identifying modulators
                                                                                             WPI; 2004-544089/52.
N-PSDB; ADQ89611.
                                                                                                                                                                                                                                                                                                            Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                            Antagonist of cell cycle progression polypeptide #21
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADQ89612 standard;
                                                                                                                                                                                      10-JAN-2003; 2003US-0439123P
06-MAY-2003; 2003US-0468402P
                                                                                                                                                                                                                               31-DEC-2003; 2003WO-GB005635
                                                                                                                                                                                                                                                                                   WO2004063362-A2
                                                                                                                                                                                                                                                                                                                                                 Cytostatic; cancer; cell
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                                                                                                                                                             (CYCL-) CYCLACEL LTD
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                           or meiosis.
SEQ ID NO 42; 461pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKGFGKHEEFPVLGQGTFYPLMIKDFNLLKWINANSFRTSHYPYSEEWLDLADRLGILVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSSLTIKNPHLWSPNDPYSYKIKIEMLEDGKTVDEYTDKIGIRTVKIVNDKILLNNHPIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGEFILENARFWSLEDPYLYPLKVELEK-----DEYTLDIGIRTISWDEKRLYLNGKPVF
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                                                                                                                                   Bell G,
                                                                                                                                                                                                                                                                                                                                      progression.
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 English
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RESULT 13
ADF28924
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AC ADF28
XX
AC ADF28
XX
DT 12-F8
XX
DE Murir

standard;

protein;

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ADF28924 st; ADF28924; 12-FEB-2004

(first entry)

Murine beta-glucuronidase

precursor

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Best Local S
Matches 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a polynucleotide for preventing, treating or diagnosing a disease in an individual. The composition or the polypeptide, polynucleotide or RNA precursor, or antibody is useful for diagnosing, preventing or treating diseases (e.g. cell proliferative diseases such as cancer) in an individual. These may also be used for identifying substances capable of binding to or modulating the function of the polypeptide, capable of affecting the function of the corresponding gene, or capable of affecting the cell division cycle or cell cycle progression, preferably mitosis and/or meiosis. The present sequence represents an antagonist of cell cycle progression protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                     QMFSBEYQAELVEKTIRL---LLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVFTRDR
                                                                                                                                                                                          RLKVGIRTLSWNSQQFLINGKEVYFRGFGRHEDSDIRGKGLDNALMVRDFNLLKWIGANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTDNLRDHVGTVWYDRKFFVPRSWSKDQRIWLRFGSVHYEAYVWINGQKVVKHEMGHLPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YQD-LCYEEGPFTYKTTFYVPKXLSQ-KHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MLYPRESETREVRSLDGIWNFVRSDQANPTQGVRDEWYAKELSKSRPTIPMPVPASYNDI
                              OPKLVAHVLRR
                                                               YVWSEEFQTEVFSRHFKAFDELRKKGWFIGEFVWNFADFKTAQSYTRVGGNKKGVFTRAR
                                                                                                                                                IVCVNRYYGWYIYQGRIEEGLQALEKDIEELYA----RHRKPIFVTEFGADAIAGIHYDPP
                                                                                                                                                                                                                        SVIMWSVANEPESNHPDAEGFFKALYETANEMDRTRPVVMVSMMDAPDERTRDVALKYFD
                                                                                                                                                                                                                                                                                        FRISHYPYSEEWLDLADRLGILVIDEAPHVGITRYHYNPETQKIAEDNIRRMIDRHKNHP
                                                                                                                                                                                                                                                                                                                                                        TLDIGIRTISWDEKRLYLNGKPVFLKGFGKHEEFPVLGQGTFYPLMIKDFNLLKWINANS
                                                                                                                                                                                                                                                                                                                                                                                                                     LGEEEKKI----RTSNRFVEGEFILENARFW-----SLEDPYLYPLKVELEK-----DEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                      YAGIHRSVHLYTTPRTFIEEVEVTTNLSK-DATVGEVFYSVSVNGSAANBADNVLQIQAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YGGIIRPVLIEFTDHARILDIWVDTSESEPEKKLGKVKVKIEVSEEAVGQ-----EMTIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAEVTDLLSYGAENRITVMCDNALIQTTVPQGRITEVPNDGGMTI-----VQSYTFDFFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVDVTGKVKSG-ENELRVVVENRLKVGGFP----SKVPDSGTHTVGFFGSFPPANFDFFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MVRPQRNKKRFILILNGVWNL-------EVTSKDR---PIAVPGSWNEQ
QPKAAAHLLRK
                                                                                                                              IISFNRYNAWYSNAGRLD
                                                                                                                                                                                                                                                          YRTSHYPYSEESMQFADEHGIMIIDECPSVDTE--NFSQELLGKHKSSLEQLIHRDRNHP
                                                                                                                                                                                                                                                                                                                                                                                        LYDKDGILVANATSDQKLGGKLQVNPVKPWWPYLMHSEPGYLYQLEIKLLATNDELLDVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative 122;
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629
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Pred. No. 5.3e-65;
                                                                                                                            -MITONVIDBAIAWNKRYNKPIIMSEYGADTLEGLHMQPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                              therapeutic protesh that can be encoded by an adeno-associated virus (AAV) vector of the invention. Such vectors comprise a promoter operably positioned upstream of a nucleic acid encoding a biologically-active therapeutic mammalian serpin or cytokine polypeptide, and optionally also include an enhancer sequence and a post-transcriptional regulatory sequence. A recombinant AAV virion comprising the vector, and a mammalian cell (preferably an endothelial, islet, hepatocyte, pancreas, kidney, muscle, spleen, liver, heart, lung, or brain cell) comprising the vector are claimed. A claimed composition comprises the vector, the recombinant AAV virion, AAV viral particles, or the mammalian cell, and is used in cancer, diabetes, autoimmune disease, pancreatic disease or liver disease therapy. The composition is also used in claimed methods for preventing type I diabetes, and for reducing the rate of disease progression of type
                                                                                                                                                                                                                                                                                 Sequence 648 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New adeno-associated viral vector, useful in preparing a composition for treating or preventing e.g., cancer, diabetes, or autoimmune, pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Хeу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of murine beta-glucuronidase precursor -D-glucuronoside glucuronosohydrolase). This is an example of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Atkinson MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; SEQ ID NO 23; 183pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-2003; 2003WO-US012324
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                                                                                                                                                                                                                                              Similarity
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QEMTIKLGEEKKIRTSNRFVEGEFILENARFW----SLEDP-YLYPLKV----ELEKD
                                                            PPANFDFFPYGGIIRPVLIEFTDHARILDIWVDTSESEPEKKLGKVK--VKIEVSEEAVG
                                                                                                           LPFEVDVTGKVKSG---ENELRVVVENRLKVGGFPSKVP-----DSGTHTVGFFGSF
                                                                                                                                   TQEAALRDFIGWVWYEREAILPRRWTQDTDMRVVLRINSAHYYAVVWVNGIHVVEHEGGH
                                                                                                                                                                                 MLFPKESPSRELKALDGLWHFRADLSNNRLQGFEQQWYRQPLRESGPVLDMPVPSSFNDI
                                                                                                                                                                                                         MVRPQRNKKRFILILNGVWNLEV-TSKDR----------PIAVPGSWNEQ
                                    QDTSFDFFNYAGLHRSVVLYTTPTTYIDDITVITN---VEQDIGLVTYWISVQGSEHF--
                                                                                    LPFEADISKLVQSGPLTTCRITIAINNTLT----PHTLPPGTIVYKTDTSMYPKGYF--V
                                                                                                                                                          YQDLCYEE--GPFTYKTTFYVPKXLSQ---KHIRLYFAAVNTDCEVFLNGEKVGENHIEY
                                                                                                                                                                                                                                                                                                         in a
                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Flotte TR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                         human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        onidase; gene therapy; cytostatic; antidiabetic;
hepatotropic; adeno-associated virus.
                                                                                                                                                                                                                               30.1%; Score 902.5; DB 7; 35.7%; Pred. No. 8.3e-65; Five 103; Mismatches 207;
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RESULT 14
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                                   Use of recombinant adeno-associated virus, comprising gene encoding a protein defective or missing in lysosomal storage disease, in the manufacture of a medicament for treating the lysosomal storage disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine; adeno-associated viral expression vector; AAV; gene the lysosomal storage disease; LSD; mucopolysaccharidoses VII; MPS Sly syndrome; beta-glucuronidase; GUS; glycosaminoglycan; GAG
 Disclosure;
                                                                                                                N-PSDB; AAD06387.
                                                                                                                                                                                                               (AVIG-)
                                                                                                                                                                                                                                                                     17-NOV-1999;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE02444 standard;
                                                                                                                                      WPI; 2001-343814/36
                                                                                                                                                                        Podsakoff G,
                                                                                                                                                                                                                                                                                                                              17-NOV-2000; 2000WO-US031688
                                                                                                                                                                                                                                                                                                                                                                  25-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                         WO200136603-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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                                                                                                                                                                                                           AVIGEN INC.
CHILDREN'S HOSPITAL MEDICAL CENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDERTRDVALKYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHRKPIFVTEFGA
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 Page 85-87; 97pp;
                                                                                                                                                                                                                                                                     99US-0166097P
2000US-0215430P
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                                                                                                                                                                          Watson G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Signal_peptide
27. .648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Murine mature beta-glucuronidase (GUS)"
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                                                                                                                                                                          Couto LB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GUS).
English
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VII; MPS VII;
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The present invention relates to recombinant adeno-associated virus (AAV)

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RESULT 15
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AC ABB70
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Best Local S
Matches 224
                              Drosophila; developmental biology; cell
                                                           Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression vectors and virions, which include genes coding for enzymes defective or missing in lysosomal storage disease (LSD). AAV is useful in the manufacture of a medicament for treating lysosomal storage disease e.g., mucopolysaccharidoses VII (MPS VII). MPS VII (Sly Syndrome) is due to the deficiency in the lysosomal enzyme beta-glucuronidase (GUS) which aids in the breakdown of glycosaminoglycans (GAGs). AAV is used in gene therapy. The present sequence is murine GUS protein. This sequence is
                                                                                                                                                              ABB70164 standard;
                                                                                                 26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 648 AA;
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                                                                                                                                                                                                                                                                                                                            DAIAGIHYDPPQMFSEEYQAELVEKTIRLL--LKKDYIIGTHVWAFADFKTPQNVRRPIL
                                                                                                                                                                                                                                                                           NHKGVFTRDROPKLVAHVLR-RLW 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRRMIDRHKNHPSVIMWSVANEPESNHPDAEGFFKALYETANEMDRTRPVVMVS--MMDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NSFRTSHYPYSEEVLQLCDRYGIVVIDECPGVGIVLPQSFGNESLRHHL-----EVMEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSFRTSHYPYSEEWLDLADRLGILVIDEAPHVGIT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YYTLPIGIRTVAVTKSKFLINGKPFYFQGVNKHEDSDIRGKGFDWPLLVKDFNLLRWLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EYTLDIGIRTISWDEKKLYLNGKPVFLKGFGKHEEFPVLGQGTFYPLMIKDFNLLKWINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDTSFDFFNYAGLHRSVVLYTTPTTYIDDITVITN---VEQDIGLVTYWISVQGSEHF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPANFDFFPYGGIIRPVLIEFTDHARILDIWVDTSESEPEKKLGKVK--VKIEVSEEAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPFEVDVTGKVKSG---ENELRVVVENRLKVGGFPSKVP-----DSGTHTVGFFGSF
                                                                                                                                                                                                                                            NKKGIFTRQRQPKTSAFILRERYW 623
                                                                                                                                                                                                                                                                                                           DAIPGIHEDPPRMFSEEYOKAVLENYHSVLDQKRKEYVVGELIWNFADFMTNOSPLRVIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPFEADISKLVQSGPLTTCRITIAINNTLT----PHTLPPGTIVYKTDTSMYPKGYF--V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YQDLCYEE--GPFTYKTTFYVPKXLSQ---KHIRLYFAAVNTDCEVFLNGEKVGENHIEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MLFPKESPSRELKALDGLWHFRADLSNNRLQGFEQQWYRQPLRESGPVLDMPVPSSFNDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -QLEVQLLDEGGKVVAHGTGNQGQLQVPSANLWWPYLMHEHPAYMYSLEVKVTTTESVTD
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                                                                                                                                                                                                                                                                                                                                                                        -DLGAPYVDVICVNSYFSWYHDYGHLEVIOPQLNSQFENWYKTHQKPIIQSEYGA
                                                                                                                                                              protein;
                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.0%; Score 899.5; DB 4; 35.9%; Pred. No. 1.5e-64;
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                           signalling; insecticide;
                                                             ID NO 37284.
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Best Local Sim
Matches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57377-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 643 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 37284; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WIPO at ftp.wipo.int/pub/published_pct_sequences
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DB; ABL14267.
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LLGKHKSSLEQLIHRDRNHPSVVMWSIANEPRTGSVSADSYFELVANFTRSLDKTRPITA
                                                                                                                      RLKVGIRTLSWNSQQFLINGKPVYFRGFGRHEDSDIRGKGLDNALMVRDFNLLKWIGANA
                                                                                                                                                                                                                                                                                                                                                                            TTDNLRDHVGTVWYDRKFFVPRSWSKDQRIWLRFGSVHYEAYVWINGQKVVKHEMGHLPF
                      ----EDNIRRMIDRHKNHPSVIMWSVANEPESNHPDAEGFFKALYETANEMDRTRPVVM
                                                                                       PRTSHYPYSEEWLDLADRLGILVIDEAPHVGITRYHYNPETQK-----IA-----
                                                                                                                                                     TLDIGIRTISWDEKRLYLNGKPVFLKGFGKHEEFPVLGQGTFYPLMIKDFNLLKWINANS
                                                                                                                                                                                                                   LGBEEKKI---RTSNRFVEGEFILENARFW----SLEDPYLYPLKVELEK-----DEY
                                                                                                                                                                                                                                                                                                                                             EVDVTGKVKSG-ENELRVVVENRLKVGGFP----SKVPDSGTHTVGFFGSFPPANFDFFP 152
                                                                                                                                                                                                                                                                                                                                                                                                           YQD-LCYEEGPFTYKTTFYVPKXLSQ-KHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPF
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                                                           YRTSHYPYSEESMQFADEHGIMIIDECPSVD-
                                                                                                                                                                                      LYDKDGILVANATSDQKLGGKLQVNPVKPWWPYLMHSEPGYLYQLEIKLLATNDELLDVY
                                                                                                                                                                                                                                                 YAGIHRSVHLYTTPRTFIEEVEVTTNLSK-DATVGEVFYSVSVNGSAANEADNVLQIQAN
                                                                                                                                                                                                                                                                              YGGIIRPVLIEFTDHARILDIWVDTSESEPEKKLGKVKVKIEVSEEAVGQ----EMTIK
                                                                                                                                                                                                                                                                                                              EAEVIDLLSYGAENRITVMCDNALIQTIVPQGRITEVPNDGGMTI-----VQSYTFDFFN
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2000US-00614150
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Pred. No. 2.3e-64;
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                                                         -TELSYS-DTSKGFLLMLLASIFRNFSQE
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Search Job ti	DЬ	Ş	рь	Ş	Ф	Ş
Search completed: September 1, 2005, 19:29:37 Job time : 172 secs	586 TAQSYTRVGGNKKGVFTRARQPKAAAHLLRK 616	528 TPQNVRRPILNHKGVETRDRQPKLVAHVLRR 558	526 PIIMSEYGADTLEGLHMQPAYYWSEEFQTEVFSRHFKAFDELRKKGWFIGEFVWNFADFK 585	471 PIFVTEFGADAIAGIHYDPPQMFSEEYQAELVEKTIRLLLKKDYIIGTHVWAFADFK 527	473 AIAVSNTQDKAGRSLDIISFNRYNAWYSNAGRLDMITQNVIDEAIAWNKRYNK 525	414 VSMMDAPDERTRDVALKYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHRK 470

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Perfect score:
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   Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.
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 GenCore version (c) 1993 - 2005
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JU0275
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1289.763 Million cell updates/sec
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Compugen Ltd
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132	139.5	175	179	179.5	181	191.5	191.5	194	194	256	300.5	310	312	321	321
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818	1091	891	879	900	820	832	827	237	237	785	1007	1005	1015	2233	2228
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A97668	F83928	A82755	A55881	T19689	T37230	A97545	AB2764	B85768	E90919	H72228	A30093	T31333	I39697	B95075	E97942
mannosidase AGR_C_	hypothetical prote	beta-mannosidase p	beta-mannosidase (hypothetical prote	probable beta-mann	hypothetical prote	beta-mannosidase p	partial beta-D-glu	interrupted beta-D	hypothetical prote	beta-galactosidase	beta-galactosidase	beta-galactosidase	beta-galactosidase	beta-galactosidase

ALIGNMENTS

A72300
beta-glucuronidase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: A72300
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
R;Nelson, K.E.; Clayton, R.A.; Gotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

Nature 399, 323-329, 1999

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C;Superfamily:
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A; Residues: 1-563 <ARN>
A; Cross-references: UNIPROT: Q9X0F2;
A; Experimental source: strain MSB8
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Evidence for lateral gene transfer between Archaea A;Reference number: A72200; MUID:99287316; PMID:10360571 A;Accession: A72300
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Best Local Similarity 99.8%;
Matches 562; Conservative
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NIRRMIDRHKNHPSVIMMSVANEPESNHPDAEGFFKALYETANEMDRTRPVVMVSMMDAP
                                                 KOFNLLKWINANSFRTSHYPYSBEWLDLADRLGILVIDEAPHVGITRYHYNPETQKIAED
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                                                                                                                                    LYPLKVELEKDEYTLDIGIRTISWDEKRLYLNGKPVFLKGFGKHEEFPVLGQGTFYPLMI
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                                                                                                                 LYPLKVELEKDEYTLDIGIRTISWDEKRLYLNGKPVFLKGFGKHEEFPVLGQGTFYPLMI
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Pred. No. 4.2e-197;
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A; Accession: C90485
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A; Residues: 1-570 < KUR>
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Best Local S
Matches 230
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                                                                                                                                                 GITRYHYNPETQKI-----AEDNIRRMIDRHKVHPSVIMWSVANEPESNHPDAEGF
                                                                                                                                                                                                                                            EFPVLGQGTFYPLMIKDFNLLKWINANSFRTSHYPYSEEWLDLADRLGILVIDEAP--HV 343
                                                                                                                                                                                                                                                                                                          ARFWSLEDPYLYPLKVELE-----KDEYTLDIGIRTISWDEKRLYLNGKPVFLKGFGKHE
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                                                                                                                     NISRVMSQEEIAKMFGDVKYFEKVRDTIKEMIRQHKNRPSVIMYSVMNEPPSDIREVAEF
                                                                                                                                                                                                      DFPILGKFTYGAVLVRDFYLMRKIGANSFRTSHYPYSNEHLDLADEMGFLVILEPPLCYS
                                                                                                                                                                                                                                                                                       VIPWSPDNPYLYTLIVEMYVGGNLKDSVYERIGFRDVEVKDGKIYLNGKPIFLKGFGRHE
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QALEKDIEELYARH-RKPIFVTEFGADAIAGIHYDPPQMFSEEYQAELVEKTIRLLLKKD
                                        IRREVELFKSLDSSRPVTFAS----HRSVRDLALEYVDVISLNYYHGWYTEWGDIDSGV
                                                                          FKALYETANEMORTRPVVMVSMMDAPDERTROVALKYFDIVCVNRYYGWYIYQGRIEEGL 454
                                                                                                                                                                                                                                                                                                                                                                                                             VDTSESEPEKKLGKVKVKIEVSEEAVGQEMTIKLGEEEKKI----RTSNRFVEGEFILEN
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A; ACCEBBACH. APPROVED A PROBLEM TYPE: MRNA
A; Residues: 1-648 - WAW>
A; Cross-references: UNIPROT: P12265;
A; Cross-references: allele B
A;Map position: 5
A;Introns: 70/3; 132/3; 193/2; 241/1; 303/3; 351/3; C;Superfamily: beta-glucuronidase
C;Keywords: glycosidase; hydrolase; lysosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-264,'D',266-319,'V',321-648 <DAM>
A;Residues: 1-264,'D',266-319,'V',321-648 <DAM>
A;Residues: 1-264,'D',266-319,'V',321-648 <DAM>
A;Residues: 1-264,'D',266-319,'GB:M20204; NID:g193716; PIDN:
A;Cossidues: Cossidues: CB:J02836; GB:J03035; GB:M20204; NID:g193716; PIDN:
R;Gallagher, P.M.; D'Amore, M.A.; Lund, S.D.; Ganschow, R.E.
Genomics 2, 215-219, 1988
A;Title: The complete nucleotide sequence of murine beta-glucuronidase
A;Title: The complete nucleotide sequence of murine beta-glucuronidase
A;Reference number: A29977; MUID:88284700; PMID:3397060
A;Accession: A29977
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A; Molecule type: mRNA
A; Residues: 1-232, 'T', 234-264, 'D', 266-319, 'V', 321-427, 'K', 429-615, 'L', 617-648
A; Residues: GB: M19279; NID: g193524; PIDN: AAA37697.1; PID: g309257
A; Experimental source: allele A
R; D'Amore, M.A.; Gallagher, P.M.; Korfhagen, T.R.; Ganschow, R.E.
Biochemistry 27, 7131-7140, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-264, 'D', 266-319, 'V', 321-648 <GAL>
A; Residues: 1-268; 'D', 266-319, 'V', 321-648 <GAL>
A; Cross-references: GB: J03047; NID: g193522; PINN: AAA37696.1; PII
R; Li, H.; Takeuchi, K.H.; Manly, K.; Chapman, V.; Swank, R.T.
T. Biol. Chem. 265, 14732-14735, 1990
A; Title: The propeptide of beta-glucuronidase. Further evidence the serpin superfamily.
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R;Funkenstein, B.; Leary, S.L.; Stein, J.C.; Catterall,
Mol. Cell. Biol. 8, 1160-1168, 1988
A;Title: Genomic organization and sequence of the Gus-8-
A;Reference number: I49692; MUID:88216590; PMID:2835664
A;Accession: I49692
A;Status: translated from GB/EMBL/DDBJ
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A;Residues: 1-86,'I',88-648 <WA2>
A;Cross-references: GB:M28541; NID:g193720; PIDN:AAA63308.1;
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                                                                                                                                                       A;Gene: Gus
                                                                                                                                                                                                                                                                                 A;Residues: 593-648 <LIA>
A;Note: the location of the
                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: A35798; MUID:90368633; PMID:2394691
A;Accession: A35798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    닭
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PMID:2835664
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PMID:2779578
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RESULT 4

A25047

A25047

C;Boecies: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Catcession: A25047; S00345
R;Mahhimura, Y; Rosenfeld, M.G.; Kreibich, G.; Gubler, U.; Sabatini, D.D.;
Proc. Natl. Acad. Sci. U.S.A. 83, 7292-7296, 1986
A;Title: Nucleotide sequence of rat preputial gland beta-glucuronidase cDNA
A;Reference number: A25047; MUID:87016933; PMID:3463967
A;Accession: A25047
A;Molecule type: mRNA
A,Residues: 1-648 < NIS>
A;Crose-references: UNIPROT:P06760; GB:M13962; NID:g204329; PIDN:AAA41228.1
A;Experimental source: female preputial gland
R;Powell, P.P.; Kyle, J.W.; Miller, R.D.; Pantano, J.; Grubb, J.H.; Sly, W.
Biochem, J. 250, 547-555, 1988
A;Title: Rat liver beta-glucuronidase. cDNA cloning, sequence comparisons a
A;Reference number: S00345; MUID:88183378; PMID:3355537
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;23-648/Product: beta-glucuronidase, ER-retained form #status predicted <ERMT>
;23-633/Product: beta-glucuronidase, lysosomal (default) form #status predicted
;634-648/Domain: carboxyl-terminal propeptide #status predicted <CPRO>
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35.9%; Pred.
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A;Accession: S00345
A;Mclecule type: mRNA
A;Mclecule type: mRNA
A;Residues: 'E',15-20,'L',22-486,'L',488-648 <POW>
A;Cross-references: EMBL:Y00717; NID:g56270; PIDN:CAA68705.1;
C;Superfamily: beta-glucuronidase
C;Keywords: glycosidase; hydrolase
C;Keywords: glycosidase; hydrolase
F;1-22/jomain: signal sequence #status predicted <NAT>
F;23-648/Product: beta-glucuronidase #status predicted <MAT>
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RMIDRHKNHPSVIMWSVANEPESNHPDAEGFFKALYETANEMDRTRPVVMVSMMDAPDER
                                                                                    AIAGIHYDPPQMFSEEYQAELVEKTIRLLL---KKDYIIGTHVWAFADFKTPQNVRRPIL
                                                                                                                                                                                           ----RDKNHPAVVMWSVANEPVSSLKPAGYYFKTLIAHTKALDPTRPVTFVS-----N
                                                                                                                                                                                                                                                                           FRTSHYPYSEEWLDLADRLGILVIDEAPHVGIT-----RYHYNPETQKIAEDNIR
                                                                                                                                                                                                                                                                                                                      TLPVGIRTVAVTKSKFLINGKPFYFQGVNKHEDSDIRGRGFDWPLLIKDFNLLRWLGANS
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                                                             AVSGLHEDPPRMFSEEYQTALLE-NYHLILDEKRKEYVIGELIWNFADFMTNQSPLRVTG
                                                                                                                            TRYDADMGAPYVDVICVNSYLSWYHDYGHLEVIQLQLTSQFENWYKMYQKPIIQSEYGAD
                                                                                                                                                          TR----DVALKYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHRKPIFVTEFGAD
                                                                                                                                                                                                                                                        FRTSHYPYSEEVLOLCDRYGIVVIDECPGVGIVLPQSFGNVSLRHHL-----EVMDELVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TQEAELRNFIGWVWYEREAVLPQRWTQDTDRRVVLRINSAHYYAVVWVNGIHVVEHEGGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -QYQDLCYEEGPFTYKTTFYVPKXLSQKHIRLYFAAVNTD---CEVFLNGEKVGENHIEY
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B; Mismatches
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Science 277, 1453-1462, 1997
A;Title: The complete genome as
A;Reference number: A64720; MU
A;Accession: C64918
A;Status: nucleic acid sequence
A;Molecule type: DNA beta-glucuronidase (EC 3.2.1.31) uidA - Escherichia coli (strain K-12) N;Alternate names; beta-D-glucuronoside glucuronosohydrolase; gusA pro C;Species: Escherichia coli (strain K-12) Date: 30-Jun-1988 #sequence revision 05-Dec-1997 #text_change 09-Jul C;Date: 30-Jun-1988 #sequence revision 05-Dec-1997 #text_change 09-Jul C;Accession: C64918; IS3717; A26487; S43555 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, A.; Rose, D.J.; Mau, B.; Shao, Y. RESULT 5
GBECGC
beta-glucuronidase sequence e sequence of E MUID:97426617; not shown; Escherichia coli 7; PMID:9278503 translation not showr Burland, V.; Riley, 09-Jul-2004 protein

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A;Status, F----
A;Molecule type: DNA
A;Residues: 1,'V',3-603 <PUN>
A;Cross-references: EMBL:232701; NID:g475168; PID:g475169
A;Cross--- mhie acid hydrolase catalyzes the cleavage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-603 <BLAT>
A;Cross-references: UNIPROT:P05804; GB:AE0000257; GB:U00096; NID:g1787898;
A;Experimental source: strain K-12, substrain MG1655
R;Schlaman, H.R.; Risseeuw, E.; Franke-van Dijk, M.E.; Hooykaas, P.J.
Gene 138, 259-260, 1994
A;Title: Nucleotide sequence corrections of the uida open reading frame en
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, April 1994 A; Reference number: S43555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Jefferson, R.A.; Burgess, S.M.; Hirsh, D.
Proc. Natl. Acad. Sci. U.S.A. 83, 8447-8451, 1986
A;Title: Beta-glucuronidase from Escherichia coli as a (
A;Reference number: A26487; MUID:87041472; PMID:3534890
A;Accession: A26487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: I53717; MUID:94171050; PMID:8125312
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A; Residues: 1-419, 'VHGNIS', 427-603 <JEF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:S69414; NID:g545893; PIDN:AAB30197.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: translated from GB/EMBL/DDBJ
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Best Local Similarity
Matches 205; Conserv
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                                           WSVANEPESNHPDAEGFFKALYETANEMDRTRPVVMVSMM--DAPDERTRDVALKYFDIV
                                                                                                                                                                             FYFTGFGRHEDADLRGKGFDNVLMVHDHALMDWIGANSYRTSHYPYAEEMLDWADEHGIV
                                                                                                                                                                                                        VFLKGFGKHEEFPVLGQGTFYPLMIKDFNLLKWINANSFRTSHYPYSEEWLDLADRLGIL
                                                                                                                                                                                                                                                                                                                                                                                                                                          YVIAGKSVRITVCVNNELNWOTIPPGMVITDENGKKKQSYF-----HDFFNYAGIHRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EE--GPFTYKTTFYVPKXLSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEVDVTG
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                                                                                      VIDETAAVGFNLSLGIGFEAGNKPKELYSEEAVNGETQQAHLQAIKELIARDKNHPSVVM
                                                                                                                                                                                                                                                                 QGTSGTLQVVNPHLWQPGEGYLYELCVTAKSQTECDIYPLRVGIRSVAVKGEQFLINHKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNYAGNVWYQREVFIPKGWAGQRIVLRFDAVTHYGKVWVNNQEVMEHQGGYTPFEADVTP
    WSIANEPDTRPQGAREYFAPLAEATRKLDPTRPITCVNVMFCDAHTDTISDL----
                                                                                                                                                                                                                                                                                                          RFVEGEFILENARFWSLEDPYLYPL----KVELEKDEYTLDIGIRTISWDEKRLYLNGKP
                                                                                                                                                                                                                                                                                                                                                        VMLYTTPNTWVDDITVVTHVAQ----DCNHASVDWQV----VANGDVSVELRDADQQVVATG
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beta-glucuronidase (EC 3.2.1.31) precursor - human (,Species: Homo sapiens (man) (,Species: A26581; A40337; A24983; A36538 (,Accession: A26581; A40337; A24983; A36538 (,Accession: A26581; A40337; A24983; A36538 (,Accession: A26581; Miller, R.D.; Hoffmann, J.W.; Powell, P.P.; Grubb Proc. Natl. Acad. Sci. U.S.A. 84, 685-689, 1987 (,Artitle: Cloning, sequencing, and expression of cDNA for human beta-glucurous, Reference number: A26581; MUID:87118233; PMID:3468507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 520-585 <GUI>
A;Residues: 520-585 <GUI>
A;Crose-references: GB:M10618; NID:g183704; PIDN:AAA52621.1; PID:g183705
R;Tomatsu, S.; Fukuda, S.; Sukegawa, K.; Ikedo, Y.; Yamada, S.; Yamada, Nan. J. Hum. Genet. 48, 89-96, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M65002; NID:g183706; PIDN:AAA526 R;Guise, K.S.; Korneluk, R.G.; Waye, J.; Lamhonwah, A.M Gene 34, 105-110, 1985 A;Reference number: A24983; MUID:85232043; PMID:3924735 A;Recession: A24983
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                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: beta-glucuronidase
C;Keywords: glycoprotein; glycosidase; homotetramer; hydrolase; lysosome
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-651/Product: beta-glucuronidase, placental #status predicted <WAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P08236; GB:M15182; NID:g183232; PIDN:AAA52561.1; PID:g183233 A;Experimental source: placenta R;Shipley, J.M.; Miller, R.D.; Wu, B.M.; Grubb, J.H.; Christensen, S.G.; Kyle, J.W.; Sly Genomics 10, 1009-1018, 1991 Wu, B.M.; Grubb J.H.; Christensen, S.G.; Kyle, J.W.; Sly A;Title: Analysis of the 5' flanking region of the human beta-glucuronidase gene. A;Reference number: A40337; MUID:92009900; PMID:1916806
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A; Residues: 378-385,616-621,643-651
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A; Residues: 1-70 <SHI>
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A; Residues: 1-651 < OSH>
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LPFEVDVTGKVKSG--ENELR--VVVENRLKVGGFPSKVP---
                                                  SQDWRLRHFVGWVWYEREVILPERWTQDLRTRVVLRIGSAHSYAIVWVNGVDTLEHEGGY
                                                                                                      YQD--LCYEEGPFTYKTTFYVPKXLSQ---KHIRLYFAAVNTDCEVFLNGEKVGENHIEY 94
                                                                                                                                                           MLYPQESPSRECKELDGLWSFRADFSDNRRRGFEEQWYRRPLWESGPTVDMPVPSSFNDI
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                                                                                                                                                                                                                                                                     105;
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                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                    DB 2;
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RESULT 7

A85768

partial beta-D-glucuronidase [imported] - Escherichia coli (strain (C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-:
C;Accession: A85768
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Pott
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85768
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-368 <STO>
A;Cross-references: UNIPROT:08X671; GB:AE005174; NID:912515602; PIDN
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: uidA_1
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        HPDAEGFFKALYETANEMDRTRPVVMVSMM--DAPDERTRDVALKYFDIVCVNRYYGWYI
                                              NLSLGIGFEAGNKPKELYSEEAVNGETQQAHLQAIKELIARDKNHPSVVMWSIANEPDTR
                                                                                                                               DADLRGKGFDNVLMVHDHALMDWIGANSYRTSHYPYAEEMLDWADEHGIVVIDETAAVGF
                                                                                                                                                                                                              NPHLWQPGEGYLYELYVTAKSRTECDIYPLRVGIRSVAVKGEQFLINHKPFYFTGFGRHE
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                                                                                  TRYHYNPETOKIAEDNIRRMIDRHKNHPSVIMWSVANEPESN
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Pred. No. 1e-39;
2; Mismatches 1
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probable beta-galactosidase (EC 3.2.1.23) [imported] - Sinorhizobium meliloti C;Species: Sinorhizobium meliloti C;Species: Sinorhizobium meliloti C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 C;Accession: D95842 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F. Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001 A;Title: The complete sequence of the 1,683-bb pSymB megaplasmid from the N2-f A;Accession: D95842; MUID:21396508; PMID:11481431 A;Accession: D95842 A;Status: preliminary
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A; Experimental source: strain O157:H7, substrain C; denetics:
A; Senetics:
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DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D90919
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A;Molecule type: DNA
A;Residues: 1-370 <HAY>
A;Cross-references: UNI
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: D90919
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
301
                                                                                                                                               185
                                                                                                                                                                                                                                                                                                                                                                                                        230 NARFWSLEDPYLYPL----KVELEKDEYTLDIGIRTISWDEKRLYLNGKPVFLKGFGKHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183
                                                                                                                                                                                                                                                                                                                                                                                                                                              141;
                                                                                                                                                                                                                                                                                             65 DADLRGKGFDNVLMVHDHALMDWIGANSYRTSHYPYAEEMLDWADEHGIVVIDETAAVGF
                                                                                                                                                                                                                                                                                                                                                                     σ
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HRVFDRVSAVVGEQVWNFADFATSQGILRVGGNKKGIFTRDRKPKSAAFLLQKRWT
                          IRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVFTRDRQPKLVAHVLRRLWS
                                                                                             YQGRIEEGLQALEKDIEELYARHRKPIFVTEFGADAIAGIHYDPPQMFSEEYQAELVEKT
                                                                                                                                                                            HPDAEGFFKALYETANEMDRTRPVVMVSMM--DAPDERTRDVALKYFDIVCVNRYYGWYI
                                                                                                                                                                                                                  NLSLGIGFEAGNKPKELYSEEAVNGETQQAHLQAIKELIARDKNHPSVVMWSIANEPDTR
                                                                      QSGDLETAEKVLEKELLAWQEKLHQPIIITEYGVDTLAGLHSMYTDMWSEEYQCAWLDMY
                                                                                                                                             PQGAREYFAPLAEATRKLDPTRPITCVNVMFCDAHTDTISDL----FDVLCLNRYYGWYV
                                                                                                                                                                                                                                                                                                                  NPHLWQPGEGYLYELYVTAKSRTECDIYPLRVGIRSVAVKGEQFLINHKPFYFTGFGRHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRLLLKKDYIIGTHVWAFADFKTPONVRRPILNHKGVFTRDROPKLVAHVLRRLWS 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSGDLETAEKVLEKELLAWQEKLHQPIIITEYGVDTLAGLHSMYTDMWSEEYQCAWLDMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YQGRIEEGIQALEKDIEELYARHRKPIFVTEFGADAIAGIHYDPPQMFSEEYQAELVEKT 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PQGAREYFAPLAEATRKLDPTRPITCVNVMFCDAHTDTISDL----FDVLCLNRYYGWYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HRVFDRVSAVVGEQVWNFADFATSQGILRVGGNKKGIFTRDRKPKSAAFLLQKRWT
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Pred.
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No. 1e-39;
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RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                              125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 370;
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N2-fixing

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F.J.;

Hernan

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A; Molecule type: DNA
A; Residues: 1-755 < KURS
A; Cross-references: UNIPROT: Q92XF7; GB: AL591985; PIDN: CAC48404.1; PID: g15139876; GSPDB: GA; Excoss-references: UNIPROT: Q92XF7; GB: AL591985; PIDN: CAC48404.1; PID: g15139876; GSPDB: GA; Experimental source: strain 1021, megaplasmid pSymB
A; Experimental source: strain 1021, megaplasmid pSymB
A; Rabola, P.; Ampe, F.; Barloy-Hubler, R.Galibert, F.; Finan, T., Long, S.R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; pela, D.; Chain, P.; Cowie, T.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Reference number: A96039; MUID: 21368234; PMID: 11474104
beta-galactosidase (EC 3.2.1.23) - Thermoanaerobacterium thermosulfurigenes C;Species: Thermoanaerobacterium thermosulfurigenes C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
                                                             RESULT
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C;Superfamily: be
C;Keywords: glyco
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Best Local S
Matches 155
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;Keywords: glycosidase; hydrolas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPIAVPGSWNE----QYQDLCYEEGPFTYKTTFYVPKXLSQKHIRLYFAAVNTDCEVFLN
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                                                                                                                                                                                                                   VLNAAYGDPGISGAIGWCMFDYNT
                                                                                                                                                                                                                                                         LLKKDY---
                                                                                                                                                                                                                                                                                          ANRPRIALRPOQECTGLPRKVPYLITEFGG-----HMYPTKIYDQEQRQAEHVRRHLE-
                                                                                                                                                                                                                                                                                                                                                                                                                                              GEEWKQEAIRNVRRMIERDWNHPSIVIWGVRINESQDSH----DFYAETNRLARELDPTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --GRIDYLTYAGIYRDVWLKVTDPVSIANIKIETRDVLSDTKAVSLRCDLSNPQGLSFSG
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                                                                                                                                                                                                                                                                                                                                  RHRK----
                                                                                                                                                                                                                                                                                                                                                                                                         PVVMVSMMDAPDERTRDVALKYFDIVCVNRYYGWYIYQGRIEEGLQALEKDI---EELYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FYPLMIKDFNLLKW-INANSFRTSHYPYSEEWLDLADRLGILVIDEAP---HVGITRYHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVLYVIEVELRTGOGSDCFAAHFGFRTAEFTTEGFRLNGRPLKIRGLNRHOSFPYVGYAM
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25.7%;
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Pred.
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No. 2.5e-25;
                                                                                                                                                                                                                   HKDFGSGDRICYHGVMDMFREPKFAA
                                                                                                                                                                                                                                                                                                                                                                     YITDSEFLEDVYTMNDFILGNEELPG
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RESULT 11 D86872

beta-galactosidase (EC 3.2.1.23) [imported] - C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-

23-Mar-2001 #text_change 03-Aug-2001

Lactococcus lactis subsp.

lactis

(strain

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A;Molecule type: protein A;Residues: 1,'X',3-27 <EC;Genetics:
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A; Molecule type: DNA
A; Residues: 1-716 <BUR>
A; Cross-references: UNIPROT: P26257;
A; Cross-references: Btrain EM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: lacZ
C;Superfamily: beta-galactosidase
C;Keywords: glycosidase; homodimer; hydrolase
F;389,429,462/Active site: Glu, Tyr, Glu #stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: JU0275; JT0963
R;Burchhardt, G.; Bahl, H.
Gene 106, 13-19, 1991
A;Title: Cloning and analysis of the beta-galactosidase-encoding
A;Reference number: JU0275; MUID:92039055; PMID:1840542
A;Accession: JU0275
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                                                          RHLRIQNASYLDDSISGAIGWCAFDYNT-
                                                                                                                                                                                                                                                                      DLADRIGILVIDEAPHVGITRYHYNPETQKIAEDNIRRMIDRHKNHPSVIMWSV-ANEPE
                                                                                                                                                                                                                                                                                                                                  RLYLNGKPVFLKGFGKHEEFPVLGQGTFYPLMIKDFNLLK-WINANSFRTSHYPYSEEWL
                                                                                                                                                                                                                                                                                                                                                                  TYLDAVKDVYSFNIENLKDIKLWDVDNPNLYEIKVGMKINNFSDEYDNKFGFREAVFKPD
                                                                                                                                                                                                                                                                                                                                                                                              RFVEG-----EFILEN---ARFWSLEDPYLYPLKVELE----KDEYTLDIGIRTISWDEK
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KFASYVYK
                          KLVAHVLR
                                                                                      KTIRL---LLKKDYIIGTHVWAFADFKTPQNVRRPILNHK------
                                                                                                                      FNDFIHDGINKPLRKQQEVTGLEHNVPYLVTEYNG-----HMYPTKRFDNEERQMEHCL
                                                                                                                                                 YQGRIEEGL-QALEKDIEELYARHRKPIFVTEFGADAIAGIHYDPPQMF-SEEYQAELVE
                                                                                                                                                                                                             SNHPDAEGFFKALYETANEMDRTRPVVMVSMMDAPDERTRDVALKYFDIVCVNRYYGWYI 445
                                                                                                                                                                                                                                          NKCDELGLLVFEEIPG---WQYIGNSEWKKVAEQNLREMITRDWNHPSIILWGVRINESQ
                                                                                                                                                                                                                                                                                                      GFYLNGRKLKLRGLNRHQSYPYVGYAMPRRVQEKDAEILKNELHLNIVRTSHYPQSKHFL
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                                                                                                                                                                               DDDAFYKNMNKIAHEIDPTROTGGVRYI----
                            557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -YFKADYEEGYEKVDDLRSFENVNLPHTNIELPYNYFDEKMYQIKSCYKYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 482; DB 2
Pred. No. 5e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GQIDYLTYGGIYREVSLGIYDDVFIKNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NID:g144838;
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                                                                                                                                                                                  -TNSSFLE--
                                                          HKDFGSGDRICYHGVMDMFRLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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                                                                                        -GVFTRDRQP
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C; Accession: D86872
R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; We Genome Res. 11, 731-753, 2001
A; Title: The complete genome sequence of the lactic acid bacterium L A; Reference number: A86625; MUID:21235186; PMID:11337471
A; Accession: D86872
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-996 <STO>
A; Cross-references: GB:AEE005176; PID:g12725024; PIDN:AAK06078.1; GSP A; Cross-references: GB:AEE005176; PID:g12725024; PIDN:AAK06078.1; GSP A; Experimental source: strain IL1403
C; Superfamily: beta-galactosidase
C; Keywords: glycosidase; hydrolase
RESULT 12
F72283
F72283
beta-galactosidase - Thermotoga maritima (strain MSB8)
beta-galactosidase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: F72283
C;Accession: F72283
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, Garrett, M.M.;
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Best Local S
Matches 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLGILVIDEA---PHVGIT---RYHYNPETQKIAEDNIRRMIDRHKNHPSVIMWSVANEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECHGF-DAEIGVVNPKLWSDEIPYLYRLELTLMDRSGAVFHKETKKIGIRKIAIEKGQLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNGVWN-----LEVTSKDRPIAVPGSWNEQYQDLCYEEGPFTYKTTF----
                                                                                                                                                                                                                                                                         ILNHKGVFTRDRQPK
                                                                                                                                                                                                                                                                                                                                                        POMFSEEYQAELVEKTIRLLLKKDYIIGTHVWAF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --ESNHPDAEGFFKALYETANEMDRTRPVVMVSMMDAPDERTRDVALKYFDIVC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EYGLYVMDEANIETH-GMTPMNRLTNDPTYLPLMSERVTRMVMRDRNHPSIIIWSLGNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INGKALLVRGVNKHEFTPEHGYVVSEEVMIKDIKLMKEHNFNAVRCSHYPNDSRWYELCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSNRFVEGEFILENARFWSLEDPYLYPLKVELEK-----DEYTLDIGIRTISWDEKRLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPVLIEFTDHARILDIWVDTSESEPEKKLGKVKVKIEVSEEAVGQE-MTIKLGEEEKKIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFDISNLAKEGONCLKVLVFRWSKVTYFEDQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVDVTGKVKSGENELRVVVENRLKVGGFPSKVPDSGTHTVGFFGSFPPANFDFFPYGGII 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QPPYVPEANPVGAYSRYFDITKEWLESGHVHLTFEGVGSAFHFWLNGEYGGYSEDSRLPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNGLWNFDHFSRISDVPKNWLELTESKTEIIVPSNWQIEFKD--KSDVPIYTNVTYPIPI
                                                                                                                                                                                                                                                                                                                  ---FGKYWQA-----FREIDRLQGGFIWDWVDQGLLKDGNYAYGGDFGDKPNDRQF
                                                                                                                                                                                                                                                                                                                                                                                                   DSPSINAPYSLKTWMG--
                                                                                                                                                                                                                                                                                                                                                                                                                                        ---- VNRYYGWYIYOGRIEEGLQALEKDIEELYARHRKPIFVTEFGAD---- AIAGIHYDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNGKPVFLKGFGKHEEFPVLGQGTFYPLMIKDFNLLKWINANSFRTSHYPYSEEWLDLAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSVNLQWLPDNYLLDFSIKT---DLDEDLDFANVKLQAYAKNIDDACLEFKLYDDEQLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---YVPKX-----LSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                    GLVFPNROAK
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                                                                                                                                                                                                                                    578
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Pred. No. 8.7e-
91; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e 481.5; DB 2;
. No. 8.7e-25;
ismatches 209;
                                                                                                                                                                                                                                                                                                                                                                                                 ----VAGENRPLILCEYAHDMGNSLGG-----
                                                                                                                                                                                                                                                                                                                                                        -----ADFKTPQNVRRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                             Hickey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ehrl
                                    beta-galactosidase (EC 3.2.1.23) lacZ [validated] - Escherichia N,Alternate names: beta-D-galactosidase; lactase C,Species: Escherichia coli C;Date: 24-Apr-1984 #sequence_revision 23-Sep-1997 #text_change C,Accession: A90981; A92233; A93224; S06878; I41218; H64761; I40 R;Kalnins, A.; Otto, K.; Ruther, U.; Muller-Hill, B. EMBO J. 2, 593-597, 1983
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A;Title:

Sequence of the lacZ gene of Escherichia coli

coli

(strain

09-Jul-2004)987; A00898;

S14637;

S14

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C;Genetics:
A;Gene: TM1193
C;Superfamily: beta-galactosidase
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Best Local S
Matches 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163;
                                                                                                486
                                                                                                                                 481
                                                                                                                                                                                                    433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLTDVLRPGKNLITVEV--
                             GVFTRDROPKLVAHVLRRLWSEV
                                                                DYWDVIEKYPYLHGGCIWDWVDQGIR---
                                                                                                -HYDPPQMFSEEYQA---ELVEKTIRLLLKKDYIIGTHVWAF-ADFKTPQNVRRPILNHK
                                                                                                                                                               PDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYA--RHRKPIFVTEFG---ADAIAGI-
                                                                                                                                                                                                                                  HPSVIMWSVANEPESNHPDAEGFFKALYETANEMDRTRPVVMVSMMDAPDERTRDVALKY
                                                                                                                                                                                                                                                                                                                                                              RTISWDEKRLYLNGKFVFLKGFGKHEEFFVLGQGTFYFLMIKDFNLLKWINANSFRTSHY
                                                                                                                                                                                                                                                                                                                                                                                                       LITPDGDEKTLVKETVKPEDRVLSFAFDVKDPKKWSAETPHLYVLKLKLGEDEKKVNFGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLIEFTDHARILDIWVDTSESEPEKKLGKVKVKIEVSBEAVGQEMTIKLGBEEKK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVTGKVKSGENELRVVVENRLKVGGFPSKVPDSGTHTVGFFGSFPPANFDFFPYGGIIRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNGNWRFLFAKNPFEVPEDFFSEKFDDSNWDEIEVPSNWEMKGYGKPIYTNVVYPFEPNP
GVVLPDRTPEPELYEVKKVYQNV
                                                                                                                                     VDVF-----
                                                                                                                                                                                                                                                                     PNOTKWYDLCDYFGLYVIDEA-NIESHGIDWDPEVTLANRWEWEKAHFDRIKRMVERDKN
                                                                                                                                                                                                                                                                                                   PYSEEWLDLADRLGILVIDEAPHVGITRYHYNPET-----OKIAEDNIRRMIDRHKN
                                                                                                                                                                                                                                                                                                                                        RKIEIKDGTLLFNGKPLYIKGVNRHEFDPDRGHAVTVERMIQDIKLMKQHNINTVRTSHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VYLYALPKFHIRDVFVRTDLDENYRN-GKIFLDVEMR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFVPKDDNPTGVYRRWIEIPEDWFKKEIFLHFEGVRSFFYLWVNGKKIGFSKDSCTPAEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -TYKTTFYVPKXLSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                            -IRTSNRFVEGEFILENARFWSLEDPYLYPLKVELEKDEYTLDIGI
:: :| : | ::: : || | |:|| ||::| ::|
                                                                                                                                                                                                    -GDGVNFEKAAL-WIKKRDNTRLIHY-----EGTTRRGESYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97;
                                                                                                                                 ----SLMYPKMDILLEYASKKREKPFIMCEYAHAMGNSVGNLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 452.5; DB 2
Pred. No. 9.4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                               563
                                                                  KKDE-NGREFWAYGGDFGDTPNDGNFCIN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----NLGEEEEKDLEVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141;
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                                                                                                  540
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A;Reference number: A58594, MUID:94277211; PMID:8008071
A;Contents: annotation; X-ray crystallography, 2.50 angstroms
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; E
A.; Rose, D.J.; Mau, B.; Shao, Y
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64761
                                                                                                                                                                                                                                                        A;Title: Nucleotide sequence of the classical lacZ deletion delta A;Reference number: I40987; MUID:93083990; PMID:1339377 A;Accession: I40987
                                                                                                                                                                                                                                                                                                                                                                     A;Status: .....
A;Nolecule type: DNA
A;Residues: 1-1024 <BLAT>
A;Cross-references: GB:AE000141; GB:U00096; NID:g1786532;
A;Cross-reference: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 967-971, 'R', 973-1022, 'E',1024 <MIK>
A;Residues: 967-971, 'R', 973-1022, 'E',1024 <MIK>
A;Cross-references: GB:M38327; NID:g146061; PIDN:AAA23835.1; PID:g146062
A;Cross-references: GB:M38327; NID:g146061; PIDN:AAA23835.1; PID:g146062
R;Jacobson, R.H.; Zhang, X.; Dubose, R.F.; Matthews, B.W.
A;Reference number: A65102; PDB:1BGL
A;Contents: annotation; X-ray crystallography, 2.50 angstroms, residues 4
R;Jacobson, R.H.; Zhang, X.J.; DuBose, R.F.; Matthews, B.W.
Nature 369, 761-766, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X16313; NID:g41903; PIDN:CAA34380.1; PID:g41904 R;Mikryukov, N.N.; Petrov, N.A.; Karginov, V.A.; Vassilenko, S.K. Bioorg. Khim. 6, 1735-1736, 1980
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A;Title: Molecular consequences of deletion formation mediated A;Reference number: A93224; MUID:80188189; PMID:6246435
A;Accession: A93224
                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-11,43-50 <RES>
A;Cross-references: EMBL:X58252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bioorg. Khim. 6, 1735-1736, 1980
A;Title: Nucleotide sequence of a lambda-plac 5-1
A;Reference number: 141218
A;Accession: 141218
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A;Residues: 356-476 <CAL>
A;Residues: 356-476 <CAL>
R;Ruteshouser, E.C.; Richardson, J.P.
J. Mol. Biol. 208, 23-43, 1989
J. Title: Identification and characterization of transcription A;Reference number: S06878; MUID:89362462; PMID:2475637
A;Accession: S06878
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A; Residues: 2-1024 < POW>
A; Note: this is the final paper
R; Calos, M.P.; Miller, J.H.
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A;Cross-references: UNIPROT:P00722; GB:V00296; NID:g41901;
A;Note: translation of initiator Met is not shown
                                                                                                                                                                                                                                                                                                                                           Gene 122, 231-232, 1992
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A; Residues: 1-147 < RUT>
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                                                                                     A; Map position: 8 min
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                                ; Function:
                                                           ;Complex: homotetramer
                                                                                                                                             Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: nucleic acid sequence not shown; translation not shown
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  hydrolysis of lactose
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galactose
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  and
                                                                                                                                                                        PID:940883
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C;Superfamily: beta-galactosidase
C;Koywords: glycosidase; homotetramer; hydrolase; magnesium
F;2-1024/Product: beta-galactosidase #status experimental <MAT>
F;2-50/Region: alpha complementation
F;51-218/Domain: 1, jelly-roll beta-barrel #status predicted <DM1>
F;219-334/Domain: 2, fibronectin type-III fold #status predicted <DM2>
F;335-627/Domain: 3, distorted TIM barrel #status predicted <DM2>
F;335-627/Domain: 4, fibronectin type-III fold #status predicted <DM2>
F;628-737/Domain: 5, anti-parallel beta-sandwich #status predicted <DM5>
F;417,419,462/Binding site: magnesium (Glu, His, Glu) #status experimental
F;462,504,538/Active site: Glu, Tyr, Glu #status predicted
F;462,504,538/Active site: Glu, Tyr, Glu #status predicted
                                                                                                                                                                                   R;Hayasur, ...
gasawara, N.; Yasunaga, T.; Kunara, o., ....
DNA Res. 8, 11-22, 2001
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia
                                                                                                                                                                                                                                                                                                                                 beta-D-galactosidase [imported] - Escherichia coli C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 C;Accession: E90678
A;Gene: ECs0397
C;Superfamily: beta-galactosidase
                                                                            A;Cross-references: UNIPROT:Q8X685; GB:BA000007; A;Experimental source: strain O157:H7, substrain
                                                                                                                       A; Molecule type: DNA
A; Residues: 1-1024 < HAY>
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N.; Yasunaga, T.; Kuhara,
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                                                                                                                                                                                                                                                                                      Kurokawa, K.; Ishii,
Shiba, T.; Hattori,
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RIMD 0509952
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Shinagawa,
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Best Local Sin Matches 159; Query Match

Similarity

13.5%; ilarity 25.2%; Conservative 8

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Score 405.5; DB 2 Pred. No. 1.4e-19; 8; Mismatches 216

DB 2;

Length 1024;

169;

Gaps

26;

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beta-D-galactosidase [imported] - Escherichia coli (strain O157:H7, substrain EDL9 C;Bpecies: Escherichia coli C;Bpecies: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession: A85529 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Ap Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85529
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1024 <STO>
A;Crenetice: UNIPROT:Q8X685; GB:AE005174; NID:g12513175; PIDN:AAG54693.1; GC:Genetice: 1-107
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                                                                  Similarity
LNGVWNLEVTSKDRPIAVPGSWNE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VWAF -- ADFKTPONVRRPILNHKGVFTRDROP 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYAHAMGNSLGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFG---ADAIAGIHYDPPQMFSEEYQA------ELVEKTIRLLLKKDYIIGTH
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                                                                                                                  beta-galactosidase
                                                 Conservative
                                             13.5%; Score 405.5; DB 2; 25.2%; Pred. No. 1.4e-19; tive 88; Mismatches 216;
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                                                                                                                                                                   NID:g12513175; PIDN:AAG54693.1; GSPDB: EDL933
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                                 VWAF--ADEKTPONVRRPILNHKGVFTRDRQP 549
                                                                                                                                                                                              NHPSVIIWSLGNESGHGANH-----DALYRWIKSVDPSRPVQYEGGGADTSATDIICP
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PWSAYGGDFGDTPNDRQFCMN--GLVFADRTP
                                                                EYAHAMGNSLGG----FAKYWQAFRQYPRLQGGFVWDLVDQS---LIKYDE--NGN
                                                                                               EFG---ADAIAGIHYDPPQMFSEEYQA-----ELVEKTIRLLLKKDYIIGTH
                                                                                                                                MYARVDEDQPFPAVPKWSI-----KKWLSLPGEM--
                                                                                                                                                            MMDAPDERTROVALKYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHRKPIFVT 475
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Search completed: September 1, 2005, 19:33:26 Job time: 45 secs

(Oldsu) Anola agod sirli

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Result
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Maximum DB
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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3001
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BGLR_MOUSE
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5 canis famil
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(C STRAIN=ATCC 35092 / DSM 1617 / P2;

(C STRAIN=ATCC 35092 / DSM 1617 / P2;

(X MEDLINE=21332296; PubMed=11427726; DOI=10.1073/pnas.141222098;

(X She Q., Singh R. K., Confalonieri F., Zivanovic Y., Allard G.,

(A She Q., Singh R. K., Confalonieri F., Zivanovic Y., Allard G.,

(A Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

(A Awayez M.J., Chan-Weiher C.C., Gordon P. M. K.,

(A Awayez M.J., Chan-Weiher C.C., Gordon P. M. K.,

(A Heikamp-de Jong I., Jeffriss A.C., Kozera C.J., Medina N., Peng X.,

(A Heikamp-de Jong I., Jeffriss A.C., Kozera C.J., Medina N., Peng X.,

(A Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

(A Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

(A Charlebois R.L., Bagan M.A., Sensen C.W., Van der Oost J.;

(A Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

(A Racoccad, Sci. U.S.A. 98:7835-7840(2001).

(B PIR; C90485; C90485.

(B PIR; C90485; Lebbra-Clucurolidae activity. IP)

(C) CO.00456 E. E-bbra-Clucurolidae activity. IP)

(B PIR; C90485, E-bbra-Clucurolidae activity. IP)
GO; GO:0004566; F:beta-glucuronidase activity
GO; GO:0005975; P:carbohydrate metabolism; IE
InterPro; IPR008979; Gal bind_like.
InterPro; IPR006101; Glyco_hydro_2.
InterPro; IPR006102; Glyco_hydro_2Ig.
InterPro; IPR006104; Glyco_hydro_2SB.
InterPro; IPR006104; Glyco_hydro_2TIM.
Pfam; PF00703; Glyco_hydro_2; 1.
Pfam; PF007836; Glyco_hydro_2_; 1.
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Beta-glucuronidase (GusB) (EC 3.2.1.31).
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Archaea; Crenarchaeota;
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01-OCT-2001
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Best Local Similarity
Matches 230; Conserv
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Q8XP19;
01-MAR-2002 (TrEMBLrel. 2
01-MAR-2002 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
"Complete genome sequence of
flesh-eater.";
Proc. Natl. Acad. Sci. U.S./
EMBL; AP003185; BAB79853.1;
                                                 MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799, Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
                                                                                                                                                   Clostridium perfringens.
Bacteria; Firmicutes; Clostridia;
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PRINTS; PR00132; GLHYDRLASEZ.
Complete proteome; Glycosidase; Hydrolase.
SEQUENCE 570 AA; 66795 MW; DEB2FEC8050AF189
                                                                       MEDLINE=21664373;
                                                                                       SEQUENCE F
STRAIN=13;
                                                                                                                                         Clostridium.
                                                                                                                                                                            Name=bglR; OrderedLocusNames=CPE0147;
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              99:996-1001 (2002)
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ed. No. 5.2e-58;
Mismatches 191;
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Best Local S
Matches 227
                           QBVNV4 PRELIMINARY;
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QBVNV4;
01-MAR-2002 (TrEMBLrel. 2
01-MAR-2002 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
Beta-glucuronidase.
Clostridium perfringens.
Bacteria; Firmicutes; Clc
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GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl .
GO; GO:0005975; P:carbohydrate metabolism; IEA.
Pfam; PF00703; Glyco_hydro_2; 1.
Pfam; PF02836; Glyco_hydro_2 C; 1.
Pfam; PF02837; Glyco_hydro_2 N; 1.
PRINTS; PR00122; GLHYDRLASE2.
PROSITE; PS00608; GLYCOSYL_HYDROL_F2_1; 1.
PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; UNKNOWN_1.
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                                                                      Clostridia;
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Last sequence that annotes the contract of the contra
                                                                                                                                                                                     sequence update)
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                                                                      Clostridiales; Clostridiaceae;
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RESULT 5 Q9AFA2 ID Q9AF

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Best Local S
Matches 226
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GO; GO:0004553; F:hydrolase activity, hydrolyzing O-c
GO; GO:0005975; P:carbohydrate metabolism; IEA.
Pfam; PF00703; Glyco hydro 2; 1.
Pfam; PF02836; Glyco hydro 2 C; 1.
Pfam; PF02837; Glyco hydro 2 N; 1.
Pfam; PF02837; Glyco hydro 2 N; 1.
PFINTS; PR00132; GLYCOSYL HYDROL F2 1; 1.
PROSITE; PS00713; GLYCOSYL HYDROL F2 2; UNKNOWN 1.
PROSITE; PS00608; GLYCOSYL HYDROL F2 2; UNKNOWN 1.
SEQUENCE 599 AA; 68715 MW; BBB5386A4AAAED48 CRC64
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SEQUENCE FROM
STRAIN=13;
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"Identification of Clostridium perfringens
adaptive response to oxidative stress.";
J. Bacteriol 184:2333-2343(2002).
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26; Conservative
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                    QPKLVAHVLRRLWSEV
                                                                                  DPPQMFSEEYQAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVFTRDR
                                                                                                                                   LKYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHRK-PIFVTEFGADAIAGIHY
                                                                                                                                                                                            | HPSVIMWSVANEPESNHPDAEGFFKALYETANEMD-RTRPVVMVS-MMDAPDE-RTRDVA
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KPKMIAHSLRERWINI
                                                          TVPVMFTEEYQVEYYKANHEVMDKCKNFVGEQVWNFADFATSQGIIRVQGNKKGIFTRER
                                                                                                                    ----DVLCLNRYYGWYVAGGDLEEAKRMLEDELKGWEERCPKTPIMPTEYGADTVAGLHD
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36.7%;
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Pred. No. 1.9e-55;
Pred. Mismatches 211;
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CRC64;
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Best Local S
Matches 221
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GO; GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR008979; Gal bind like.

InterPro; IPR006101; Glyco hydro_2.

InterPro; IPR006102; Glyco hydro_21G.

InterPro; IPR006103; Glyco hydro_21G.

InterPro; IPR006103; Glyco hydro_27IM.

Pfam; PF00703; Glyco hydro_27IM.

Pfam; PF00703; Glyco hydro_2; 1.

Pfam; PF02837; Glyco hydro_2, 1.

PFANTS; PR00312; GLYCOSYL HYDROL F2_1; 1.

PROSITE; PS00713; GLYCOSYL HYDROL F2_1; 1.

PROSITE; PS00703; GLYCOSYL HYDROL F2_1; 1.

PROSITE; PS00703; GLYCOSYL HYDROL F2_2; 1.
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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Staphylococcus sp. RLH1.
Bacteria, Firmicutes; Bacillales;
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HSSP; P08236; 1BHG.
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Submitted (FEB-2001)
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                             ALKYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHR----
                                                                                                                                            HKNHPSVIMWSVANEPESNHPDAEGFFKALYETANEMD-RTRPVVMVSMMDAPDERTRDV
                                                                                                                                                                                                                                                           LADRIGILVIDEAPHVGITRYHYN-------PETQKIA-----EDNIRRMIDR
                                                                                                                                                                                                                                                                                                               KFLINNKPFYFKGFGKHEDTPINGRGFNEASNVMDFNILKWIGANSFRTAHYPYSEELMR
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                                                                                    DKNHPSVVMWSTANEAATEEEGAYEYFKPLVELTKELDPQKRPVTTVLFVMATPE--TDK
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35.6%;
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EMBL/GenBank/DDBJ
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3; Mismatches
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Pred. No. 1.3e-52;
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Best Local Sim
Matches 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . R GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . R GO; GO:0005975; P:carbohydrate metabolism; IEA. R InterPro; IPR006101; Glyco hydro 2. R InterPro; IPR006102; Glyco hydro 21g. R InterPro; IPR006104; Glyco hydro 25B. R InterPro; IPR006104; Glyco hydro 27IM. R InterPro; IPR006103; Glyco hydro 27IM. R Pfam; PF00703; Glyco hydro 2; 1. R Pfam; PF02836; Glyco hydro 2; 1. R Pfam; PF02836; Glyco hydro 2 C; 1. R Pfam; PF02837; Glyco hydro 2 C; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9AHJ8;
Q9AHJ8;
01-JUN-2001
01-JUN-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appl. Environ. Micr
EMBL; AF305888; AAK
HSSP; P08236; 1BHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Russell W.M., Klaenhammer T.R.;
"Identification and cloning of gusA, encoding
from Lactobacillus gasseri ADH.";
Appl. Environ. Microbiol. 67:1253-1261(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21141841; PubMed=11229918;
DOI=10.1128/AEM.67.3.1253-1261.2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=gusA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta-glucuronidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactobacillus gasseri
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TSSLTIKNPHLWSPNDPYSYKIKIEMLEDGKTVDEYTDKIGIRTVKIVNDKILLNNHPIY
                                                                                                                                                                                                                            GE-NELRVVVENRLKVGGFP---SKVPDSGTHTVGFFGSFPPANFDFFPYGGIIRPVLIE
                                                                                                                                                                                                                                                                                                 GPFTYKTTFYVPKXLSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEVDVTGKVKS
                                        EGEFILENARFWSLEDPYLYPLKVELEK-----DEYTLDIGIRTISWDEKRLYLNGKPVF
                                                                                                                                                                                                                                                                         GDFWYQKDFFIPSFLKKKELYIRFGSVTHRAKVFINGHEVGQHEGGFLPFQVKISNYINY
                                                                                                                                                                                                                                                                                                                                                                    PIQNKYRENTLMNGTWQFETDPNSVGLDEGWNKELPDPEEMPVPGTFAELTTKRDRKYYT
                                                                                                                                                                                                                                                                                                                                                                                                              PQRNKKRFILILNGVWNLEVT-----SKDRP----IAVPGSWNE--QYQDLCYEE
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                                                                                                                                  FTDHARILDIWVDTSESEPEKKLGKVKVKIEVSEEAVGQ-EMTIKLGEEEKKIRTSNRFV
                                                                                                                                                                               DQTNRVTVLVNNELSEKAIPCGTEEILDNGQ------KLAQPYFDFFNYSGIMRNVWLL
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34.1%;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 919.5; DB 2;
Pred. No. 5.6e-52;
0; Mismatches 227;
                                                                                       YQLANNKATITYNI EANNNAEFKVTLFDNQKEVACATSKN
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                                                                                                                                                                                                                                                                                                                                                                                          A Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb L., Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
LL Apark S., Wan K., Yu C., Rubin G.M., Celniker S.;
LL Submitted (Appr-2004) to the EMBL/GenBank/DDBJ databases.

REMBL; BT012475; AAS93746.1; -.
REMBL/GenBank/DDBJ databases.

REMBL/Ge
                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 212
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Eukaryota; Metazoa; Arthropoda; Hazapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                           MLYPRESETREVRSLDGIWNFVRSDQANPTQGVRDEWYAKELSKSRPTIPMPVPASYNDI
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2; Mismatches 209;
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MEDLINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Addams M.D., Celniker S.B., Holt R.A., Evans C.A., Gocayne J.D., Addams M.D., Celniker S.B., Holt R.A., Evans C.A., Gocayne J.D., Addams M.D., Celniker S.B., Holt R.A., Hoskins R.A., Galle R.F., Addams M.D., Celniker S.B., Richards S., Ashburner M., Henderson S.N., Salton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Salton G.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., Addams K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., Abril J.F., Agbayani A., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.F., Bhandari D., Bolshakov S., Ash Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Chartis K.C., Cawley S., Dahlke C., Davenport L.B., Davies P., Cander A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K.J., Doupt J.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Adder M., Cabrista C.C., Ferrara C., Ferriera S., Fleischmann W., Posler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., Van Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update
25-OCT-2004 (TrEMBLrel. 28, Last annotation update
25-OCT-2004 (TrEMBLrel. 28, Last annotation update
CG15117-PA (LD04718p).
ORFNames=CG15117;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa, Arthropoda; Haxapoda; Insect.
Neoptera; Endopteryora; Diptera; Brachycera; Mu
Ephydroidea; Drosophilidae; Drosophila.
NCBI TaxID=7227;
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InterPro; IPR008101; Glyco hydro 2.
InterPro; IPR006102; Glyco hydro 22.
InterPro; IPR006103; Glyco hydro 25B.
InterPro; IPR006103; Glyco hydro 27IM.
InterPro; IPR006103; Glyco hydro 27IM.
InterPro; IPR006025; Pept M Zn BS.
Pfam; PF00703; Glyco hydro 2; I.
Pfam; PF00813; Glyco hydro 2; I.
Pfam; PF02834; Glyco hydro 2; I.
Pfam; PF02834; Glyco hydro 2; I.
PRINTS; PR00112; GLYCOSYL HYDROL F2 1; 1.
PROSITE; PS00719; GLYCOSYL HYDROL F2 1; 1.
PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SEQUENCE 656 AA; 75166 MW; 34168D33C8F88A
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GO; GO:0004533; F:hydrolase activity, hydro
GO; GO:0005975; P:carbohydrate metabolism;
GO; GO:0005975; Gal bind_like.
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                                                                                    QMFSEEYQAELVEKTIRL---LLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVFTRDR
                                                                                                                                                                                SVVMWSIANEPRTGSVSADSYFELVANFTRSLDKTRPITAAIAV---
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QPKAAAHLLRK
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                                                           YVWSEEFQTEVFSRHFKAFDELRKKGWFIGEFVWNFADFKTAQSYTRVGGNKKGVFTRAR
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R GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .;

R GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .;

R GO; GO:0005975; F:carbohydrate metabolism; IEA.

R InterPro; IPR008101; Glyco hydro 2:

R InterPro; IPR006101; Glyco hydro 2:IG.

R InterPro; IPR006102; Glyco hydro 2:IM.

R InterPro; IPR006103; Glyco hydro 2:IM.

DR InterPro; IPR006103; Glyco hydro 2:IM.

DR InterPro; IPR006103; Glyco hydro 2:IM.

DR Pfam; PF00703; Glyco hydro 2: C; 1.

DR Pfam; PF00703; Glyco hydro 2: N; 1.

DR Pfam; PF00703; Glyco hydro 2: N; 1.

DR Pfam; PF00837; Glyco hydro 2: N; 1.

DR PFAM; PF00837; Glyco hydro 2: N; 1.

DR PROSITE; PS00719; GLYCOSYL HYDROL F2 1; 1.

DR PROSITE; PS00742; ZINC PROTEASE; UNKNOWN 1.

SQ SEQUENCE 670 AA; 77036 MW; 7A9F23351E458C90 CRC64;
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Best Local Sim
Matches 212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE003797;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22426069; PubMed=12537572;
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                               YRTSHYPYSEESMQFADEHGIMIIDECPSVDTE--NFSQELLGKHKSSLEQLIHRDRNHP
                                                                                                     RLKVGIRTLSWNSQQFLINGKPVYFRGFGRHEDSDIRGKGLDNALMVRDFNLLKWIGANA
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                                                                FRISHYPYSEEWLDLADRLGILVIDEAPHYGITRYHYNPETQKIAEDNIRRMIDRHKNHP
                                                                                                                                    TLDIGIRTISWDEKRLYLNGKPVFLKGFGKHBEFPVLGQGTFYPLMIKDFNLLKWINANS
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                                                                                                                                                                                                                                                                                 YGGIIRPVLIEFTDHARILDIWVDTSESEPEKKLGKVKVKIEVSEEAVGQ-----EMTIK
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MEDLINE=88284700; pubMed=3397060;
Gallagher P.M., D'Amore M.A., Lund
"The complete nucleotide sequence
and its deduced polypeptide.";
Genomics 2:215-219(1988).
                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C3H/HeJ, and YBR; TISSUE=Sperm;
MEDLINE=89384641; PubMed=2779578;
MEDLINE=89384641; PubMed=2779578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P12265; Q61601; Q64473; Q64474;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Beta-glucuronidase precursor (EC 3.2.1.31)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOUSE
                                                                                                         SEQUENCE FROM N.A.
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MEDLINE=89062453; PubMed=3196706;
D'Amore M.A., Gallagher P.M., Kor
                                                                                                                                                                                                                                                                                                                                                   Gallagher P.M., D'Amore M.A., Lund S.D.,
Hohman C., Korfhagen T.R., Ganschow R.E.;
"DNA sequence variation within the beta-g
among inbred strains of mice.";
Genomics 1:145-152(1987).
                                                               Funkenstein B., Leary S.L., Stein : "Genomic organization and sequence murine beta-glucuronidase gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Gusb; Synonyms=Gus, Gus-s;
Mus musculus (Mouse).
                                                                                              MEDLINE=88216590; PubMed=2835664;
                                                                                                                                                         Wawrzyniak C.J., Gallagher P.M., D'Amore M.A., Rinchik E.M., Ganschow R.E.;
                                                                                                                                                                                                                Biochemistry 27:7131-7140(1988)
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BGLR_MOUSE
                                                                                                                                             'DNA determinants of structural and regulatory
                                                                                                                                                                                                                                   'Complete
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                                     FUNCTION: Plays an important and keratan sulfates.
  SUBCELLULAR LOCATION:
                            and keratan sulfates
CATALYTIC ACTIVITY:
                    D-glucuronate.
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                                                                                                                           beta-glucuronidase gene complex."; sll. Biol. 9:4074-4078(1989).
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                                              Biol. 8:1160-1168(1988).
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  LOCATION: Lysosomal
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D'Amore M.A., Lund S.D.,
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Rodentia;
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                             beta-D-glucuronoside
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ne Gus-s alpha
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EYTLDIGIRTISWDEKRLYLNGKPVFLKGFGKHEEFPVLGQGTFYPLMIKDFNLLKWINA
                                                                           PPANFDFFPYGGIIRPVLIEFTDHARILDIWVDTSESEPEKKLGKVK--VKIEVSEEAVG
                                                                                                                 LPFEVDVTGKVKSG---ENELRVVVENRLKVGGFPSKVP-----
                                                                                                                                    TQEAALRDFIGWVWYEREAILPRRWTQDTDMRVVLRINSAHYYAVVWVNGIHVVEHEGGH
                  -QLEVQLLDEDGKVVAHGTGNQGQLQVPSANLWWPYLMHEHPAYMYSLEVKVTTTESVTD
                                     QEMTIKLGEEEKKIRTSNRFVEGEFILENARFW----SLEDP-YLYPLKV-----
                                                         QDTSFDFFNYAGLHRSVVLYTTPTTYIDDITVITN---VEQDIGLVTYWISVQGSEHF--
                                                                                               LPFEADISKLVQSGPLTTCRITIAINNTLT----
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InterPro; IPR008979; Gal_bind_like.
InterPro; IPR006101; GlyGo hydro_2:
InterPro; IPR006102; GlyGo hydro_2:I9.
InterPro; IPR006104; GlyGo hydro_2:B.
InterPro; IPR006103; GlyGo hydro_2:II.
Pfam; PF00703; GlyGo_hydro_2: [1.
Pfam; PF02836; GlyGo_hydro_2 C; 1.
Pfam; PF02836; GlyGo_hydro_2 N; 1.
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EMBL; J02836; AAA98623.1; -.
EMBL; M63836; AAA63309.1; -.
EMBL; M28540; AAA63307.1; -.
EMBL; M28541; AAA63308.1; -.
EMBL; M19279; AAA37697.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00719; GLYCOSYL_HYDROL_F2_1; 1.
PS00608; GLYCOSYL_HYDROL_F2_2; 1.
tein; Glycosidase; Hydrolase; Lyso
                                                                       MVRPQRNKKRFILILNGVWNLEV-TSKDR-------PIAVPGSWNEQ
                                   MLFPKESPSRELKALDGLWHFRADLSNNRLQGFEQQWYRQPLRESGPVLDMPVPSSFNDI
YQDLCYEE--GPFTYKTTFYVPKXLSQ---KHIRLYFAAVNTDCEVFLNGEKVGENHIEY
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I -> T (in strain Y
HeJ).
V -> I (in strain Y
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E -> K (in allele G
F -> L (in allele G
                                                                                                                         Score 902.5; DB Pred. No. 8.1e-51
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                                                                                                                                                                               -> K (in allele GUS-SA)
-> L (in allele GUS-SA)
3D8C65A5DB3B96D6 CRC64;
                                                                                                          ed. No. 8.16
Mismatches
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SEQUENCE
STRAINSHMRI; TISSCE
Director MGC Project;
Submitted (JUN-2004) to the EMBL/Gensum.
R EMBL; BC071226; AAH71226.1; -.

OG GO:0004553; F:hydrolase activity, hydrolyz RGO; GO:0005975; P:carbohydrate metabolism; IEP InterPro; IPR008979; Gal bind like
InterPro; IPR006101; Glyco_hydro_2.

TherPro; IPR006102; Glyco_hydro_25B.
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XX MEDLINE-22388257; PubMedel12477932; DOI=10.1073/pnas.242603899;
XX MEDLINE-22388257; PubMedel12477932; DOI=10.1073/pnas.242603899;
XX Altasher R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,
XX Altasher R.D., Collins F.S., Magner L., Shensen C.F., Bhat N.K.,
XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
XX Altasher R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
XX Altasher R.F., Jordan H., Moore T., Max. S.I., Wang J., Hong L.,
XX Altasher M.J., Medin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Altasher M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Altasher S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
XX Alchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
XX Altasher S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
XX Altasher M. M. May D.M., Sodergren E.J., Lu X., Gibbs R.A.,
XX Altasher M. M. Wany D.M., Sodergren E.J., Lu X., Gibbs R.A.,
XX Altasher M. M. Wang A.C., Shevchenko Y., Bouffard G.G.,
XX Allasher M. T., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
XX Alones S.J. Marra M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel. Glucuronidase, beta.
                                                                                                                                                                                                                                                                                                                       "Generation and initial analysis and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99;
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Mammalia; Eutheria;
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Rodentia;
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BGIR FELCA STANDANCE,
097524;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
7-7-rlucuronidase precursor (EC 3.2.1.31).
                                                                           NCBI_TaxID=9685;
                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                 SEQUENCE
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FROM N.A.,

AND

VARIANT

MPS

VII LYS-351

Carnivora; Chordata;

Craniata; Vej ; Fissipedia;

Vertebrata; ia; Felidae;

Euteleostomi; Felis.

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Query Match
Best Local S
Matches 224
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Pfam; PP00703; Glyco_hydro_2; 1.

Pfam; PP02836; Glyco_hydro_2; 1.

Pfam; PP02837; Glyco_hydro_2, 1.

PRINTS; PR00132; GLYCOSYL_HYDROL_F2_1; 1.

PROSITE; PS00608; GLYCOSYL_HYDROL_F2_1; 1.

PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; 1.

PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; 1.
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NKKGIFTROROPKTSAFILRERYW
                               NHKGVFTRDRQPKLVAHVLR-RLW
                                                                      DAIPGIHEDPPRMFSEEYQKAVLENYHSVLDQKRKEYVVGELIWNFADFMTNQSPLRVIG
                                                                                                                                                                              PDERTRDVALKYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHRKPIFVTEFGA
                                                                                                                                                                                                                          VR----RDKNHPAVVMWSVANEPSSALKPAAYYFKTLITHTKALDLTRPVTFVSNAKYDA
                                                                                                                                                                                                                                                 IRRMIDRHKNHPSVIMWSVANEPESNHPDAEGFFKALYETANEMDRTRPVVMVS--MMDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      -QLEVQLLDEGGKVVAHGTGNQGQLQVPSANLWWPYLMHEHPAYMYSLEVKVTTTESVTD
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No. 1.3e-50;
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Best Local S
Matches 224
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InterPro; IPR008101; Glyco_hydro_2.
InterPro; IPR008101; Glyco_hydro_21g.
InterPro; IPR008104; Glyco_hydro_25B.
InterPro; IPR008103; Glyco_hydro_2.7IM.
Pfam; PP00803; Glyco_hydro_2.7.
Pfam; PP02836; Glyco_hydro_2.7.
Pfam; PP02836; Glyco_hydro_2.7.
Pfam; PP02837; Glyco_hydro_2.7.
Pfam; PP02837; Glyco_hydro_2.7.
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VARIANT
SEQUENCE
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SIGNAL
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUB-Liver,
MEDLINE-99296826; PubMed-10366443; DOI=10.1006/geno.1999.5825;
MEDLINE-99296826; PubMed-10366443; DOI=10.1006/geno.1999.5825;
Eyfe J.C., Kurzhals R.L., Lassaline M.E., Henthorn P.S., Alur P.R.,
Wang P., Wolfe J.H., Giger U., Haskins M.E., Patterson D.F., Sun H.,
Jain S., Yuhki N.;
"Molecular basis of feline beta-glucuronidase deficiency: an animal
model of mucopolysaccharidosis VII.";
Genomics 58:121-128(1999)
-i- FUNCTION: Plays an important role in the degradation of dermatan
and keratan sulfates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF012423; AAD01498.1; -.
EMBL; AF012424; AAD01499.1; -.
HSSP; P08236; 1BHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1; 1.
PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; 1.
Disease mutation; Glycoprotein; Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: A beta-D-glucuronoside
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Lysosomal.
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                                                           NFDFFPYGGIIRPVLIEFTDHARILDIWVDTSESEPEKKLGKVKVKIEVSEEAVGQEMTI
                                                                                          EADISKLVQSGPLASCRITIAINNTLT----PHTLPPGTILYQTDTSKYPKGYF--VQNI
                                                                                                                         EVDVTGKVKSG---ENELRVVVENRLKVGGFPSKVP-----DSGTHTVGFFGSFPPA
                                                                                                                                                       RQLRSFVGWVWYEREATLPQRWTQDLGTRVVLRIGSAHYYAIVWVNGVHVAEHEGGHLPF
                                                                                                                                                                                      --LCYEEGPFTYKTTFYVPKXLSQ---KHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPF
                                                                                                                                                                                                                                                PQRNKKRFILILNGVWNLEVT-SKDR-------PIAVPGSWNEQYQD
 KLGEEEKKIRTSNRFVEGEFILENARFW----SLEDP-YLYPLKVELE---
                             NFDFFNYAGLHRPVLLYTTPTTYIDDITISTSVNQ-DTGLVDYQIFVEGGEHF----QLEV
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E -> K (in MPS VII)
                                                                                                                                                                                                                                                                                             Score 898;
Pred. No. 1
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Proton donor (By si
                                                                                                                                                                                                                                                                                                                                            2AE30884B70D4232 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                             DB 1;
.6e-50;
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RESULT 13
BGLE RAT
ID 1988 (Rel. 0
DT 01-JAN-1988 (Rel. 0
DT 01-JAN-1988 (Rel. 0
DT 025-OCT-2004 (Rel. 4
DE Beta-glucuronidase
GN Name-Gusb) Synonyms
OS Rattus norvegicus (
CC Eukaryota; Metazoa;
OC Mammalia; Eutheria;
OX NCBI TaxID-10116;
RN SEQUENCE FROM N.A.
RC TISSUB-Preputial gl
RX MEDLINE-87016933; P
RA Nishimura Y., Rosen
RA Adesnik M., Andy R.
RC TISSUB-Vitro insert
membranes ";
RL "Nucleotide sequenc
RT and in vitro insert
RT membranes ";
RL Proc. Natl. Acad. S
RN [2]
RP SEQUENCE OF 14-648
RC TISSUB-Liver;
RT MEDLINE-88183378; P
RA POWell P.P., KYle J
RT "RAT liver beta-glu
RT ENDECLILUAR LOC.
CC -!- SUBUNIT: Homote
CC -!- SUBUNIT: Homote
CC -!- SUBUNIT: Bell
CC -!- SIMILARITY: Bell
CC -!- SIMILARIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta-glucuronidase precursor
Name=Gusb; Synonyms=Gus;
Rattus norvegicus (Rat)
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and in vitro insertion of its
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MEDLINE=87016933; PubMed=3463967;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adesnik M., Andy R.;
                                                                                                                                                                              PTM: Undergoes a post-transcriptional proteolytic cleavage n its C-terminal end, which reduces its size by approximately. The site of this cleavage has as yet not been determined. SIMILARITY: Belongs to the glycosyl hydrolase 2 family.
                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Lysosomal
                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: A beta-D-glucuronoside
                                                    SWISS-PROT entry is copyright. It een the Swiss Institute of Bioinf European Bioinformatics Institute.
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                                                                                   entry is copyright. It is produced through a collaboration iss Institute of Bioinformatics and the EMBL outstation -
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Sciurognathi; Muridae;
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CARBOHYD 62
CONFLICT 1
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SEQUENCE 648
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InterPro;
Pfam; PF00
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InterPro;
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cerPro; IPR008101; Glyco_hydro_2:
cerPro; IPR006101; Glyco_hydro_2:g.
cerPro; IPR006102; Glyco_hydro_2:g.
cerPro; IPR006103; Glyco_hydro_2:B.
cerPro; IPR006103; Glyco_hydro_2: 1.
am; pP00703; Glyco_hydro_2 C; 1.
am; pP02836; Glyco_hydro_2 C; 1.
am; pP02837; Glyco_hydro_2 N; 1.
INTS; PR00132; GLHYDRLASE2.
DSITE; PS00608; GLYCOSYL_HYDROL_P2_2; 1.
DSITE; PS00608; GLYCOSYL_HYDROL_P2_2; 1.
ycoprotein; Glycosidase; Hydrolase; Lysosome; Si
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TRYDADMGAPYVDVICVNSYLSWYHDYGHLEVIQLQLTSQFENWYKMYQKPIIQSEYGAD
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                                                                                                                            FRTSHYPYSEEVLOLCDRYGIVVIDECPGVGIVLPQSFGNVSLRHHL----
                                                                                                                                                          FRTSHYPYSEEWLDLADRLGILVIDEAPHVGIT----
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Q > E (in Ref. 2).
V -> L (in Ref. 2).
M -> L (in Ref. 2).
M -> L (in Ref. 2).
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Pred. No. 2.7e-50;
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OS Caniis
OC Mammal
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RA ARAY J.
RA COTTEC
RT COTTE
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InterPro; IPR008979; Gal bind like.

InterPro; IPR008101; Glyco hydro 2.

InterPro; IPR006101; Glyco hydro 2Ig.

InterPro; IPR006102; Glyco hydro 2SB.

InterPro; IPR006103; Glyco hydro 2TIM.

Pfam; PP00703; Glyco hydro 2; 1.

Pfam; PP02836; Glyco hydro 2 N; 1.

Pfam; PF02837; Glyco hydro 2 N; 1.

Pfam; PF02837; Glyco hydro 2 N; 1.

PRINTS; PR00132; GLYCOSYL HYDROL F2 1;

PROSITE; PS00608; GLYCOSYL HYDROL F2 2;
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018835;
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SIGNAL
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                                                                                                                                                                                                 Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF019759;
HSSP; P08236; 1E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98190525; PubMed-9521879; DOI=10.1006/geno.1997.5189; Ray J., Bouvet A., Desanto C., Fyfe J.C., Xu D., Wolfe J.H., Aguirre G.D., Patterson D.F., Haskins M.E., Henthorn P.S.; "Cloning of the canine beta-glucuronidase cDNA, mutation identification in canine MPS VII, and retroviral vector-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Beta-glucuronidase precursor (EC 3.2.1.31).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           correction of MPS VII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no we
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D-glucuronate.
SUBUNIT: Homoterramer (By similarity).
SUBCELLULAR LOCATION: Lysosomal.
SUSCEASE: Defects in GUSB are the cause type VII (MPS VII), an inherited disease cats, and dogs.
SIMILARITY: Belongs to the glycosyl hyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Plays an important and keratan sulfates (By sim: CATALYTIC ACTIVITY: A beta-D
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GLYCOSYL_HYDROL_F2_2; 1.
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STRAIN-C24; Deboeck F. De Greve H., Nguyen V., Deboeck F. Hernalsteens J.P.; Translation "T-DNA tagging of the translation Arabidopsis thaliana."; Plant Sci. 161:685-693(2001).
                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyladons; core eudicots; rosid
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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Patent No. 6641996

GENERAL INFORMATION:

APPLICANT: Richard A. Jefferson and Jorge E. Mayer

ITILE OF INVENTION: MICROBIAL -GLUCURONIDASE GENES, GEI

TITLE OF INVENTION: PRODUCTS, AND USES THEREOF

FILE REFERENCE: 190106.405C1

CURRENT APPLICATION NUMBER: US/09/270,957

CURRENT FILING DATE: 1999-03-17

NUMBER OF 520 ID NOS: 112

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6

LENGTH: 563

TYPE: PRT
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; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(563)
; OTHER INFORMATION: Xaa =
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Sequence 21, Application US/09270957

| Sequence 21, Application US/09270957
| Patent NO. 6641996
| GENERAL INFORMATION:
| APPLICANT: Richard A. Jefferson and Jorge E. Mayer ITILE OF INVENTION: MICROBIAL -GLUCURONIDASE GENES, GENTITLE OF INVENTION: PRODUCTS, AND USES THEREOF FILE REFERENCE: 190106.405C1
| CURRENT APPLICATION NUMBER: US/09/270,957
| CURRENT APPLICATION NUMBER: US/09/270,957
| CURRENT FILING DATE: 1999-03-17
| NUMBER OF SEQ ID NOS: 112
| SOFTWARE: FRSESEQ for Windows Version 4.0
| SEQ ID NO 21
| LENGTH: 563
| Type: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Thermotoga mar
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1) ... (563)
; OTHER INFORMATION: Xaa =
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APPLICANT: Jefferson, Richard A.
APPLICANT: Kilian, Andrzej
APPLICANTION: USES THEREOF
FILE OF INVENTION: USES THEREOF
FILE REFERENCE: 190106.405
CURRENT APPLICATION NUMBER: US/09/149,727
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: US 60/058,263
EARLIER FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 71
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TYPE: PRT
ORGANISM: Bacillus
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RESULT 4
US-09-270-957-2
; Sequence 2, Application US/09270957
; Betent NO. 6641996
; GENERAL INFORMATION:
APPLICANT: Richard A. Jefferson and Jorge E. Mayer
ITILE OF INVENTION: MICROBIAL -GLUCURONIDASE GENES, GENETITLE OF INVENTION: PRODUCTS, AND USES THEREOF
FILE REFERENCE: 190106.405C1
; CURRENT APPLICATION NUMBER: US/09/270,957
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 602
; TYPE: PRT
ORGANISM: Bacillus sp.
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Best Local Similarity
Matches 221; Conserv
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APPLICANT: Richard A.
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                                                              TRDROPKLVAHVLRRLWSEV 563
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                                                                                                                                                                                                                                                           VAELIDVIALNRYNGWYFDGGDLEAAKVHLR----QEFHAWNKRCPGKPIMITEYGADTVA
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   TRDRKPKLAAHVFRERWINI 595
                                                                                                                             GFHDIDPVMFTEEYQVEYYQANHVVFDEFENFVGEQAWNFADFATSQGVMRVQGNKKGVF
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Sequence 15, Application US/09270957

| Sequence 15, Application US/09270957
| Patent NO. 6641996
| GENERAL INFORMATION:
| APPLICANT: Richard A. Jefferson and Jorge E. Mayer ITITLE OF INVENTION: MICROBIAL -GLUCURONIDASE GENES, GENETITIE OF INVENTION: PRODUCTS, AND USES THEREOF FILE REFERENCE: 190106.405C1
| CURRENT APPLICATION NUMBER: US/09/270,957
| CURRENT FILING DATE: 1999-03-17
| TUBE: PRT SEQ ID NOS: 112
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 15
| LENGTH: 602
| TYPE: PRT ORGANISM: Bacillus sp.
RESULT 7
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Sequence 4, Application US/09149727

RESULT 8
US-09-149-727-8
; Sequence 8, Application
; Patent No. 6391547

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APPLICANT: Kilian, Andrzej
APPLICANTON: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 190106.405
FILE REFERENCE: US 60/058,263
EARLIER FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 4
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Best Local Similarity 35.6%;
Matches 221; Conservative 9
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                    TRDRQPKLVAHVLRRLWSEV 563
                                                                                                                                                                                   ALKYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHR-----KPIFVTEEGADAIA 483
                                                                                                                                                                                                                                                                                                                LADREGLVVIDETPAVGV---HLNFMATTGLGEGSERVSTWEKIRTFEHHQDVLRELVSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MVRPQRNKKRFILILNGVWNLEV------TSKDRPIAVPGSWNE--QYQDLC
                                                                                                                    GIHYDPPOMFSEEYOAELVEKTIRLLLKKDYIIGTHVWAFADFKTPONVRRPILNHKGVF
                                                                                                                                                          VAELIDVIALNRYNGWYFDGGDLEAAKVHLR---QEFHAWNKRCPGKPIMITEYGADTVA
                                                                                                                                                                                                                                         DKNHPSVVMWSTANEAATEEEGAYEYFKPLVELTKELDPQKRPVTIVLFVMATPE--TDK
                                                                                                                                                                                                                                                                             HKNHPSVIMWSVANEPESNHPDAEGFFKALYETANEMD-RTRPVVMVSMMDAPDERTRDV
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TRDRKPKLAAHVFRERWINI 611
                                                                             GFHDIDPVMFTEEYQVEYYQANHVVFDEFENFVGEQAWNFADFATSQGVMRVQGNKKGVF
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FILE REFERENCE: 190106.405
CURRENT APPLICATION NUMBER: US/09/149,727
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: US 60/058,263
EARLIER FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 8
LENGTH: 607
RESULT 9
US-09-270-957-18
; Sequence 18, Application US/09270957
; Patent No. 6641996
; GENERAL INFORMATION:
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Best Local Similarity
Matches 220; Conserv
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ORGANISM: Bacillus
:-09-149-727-8
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APPLICANT: Kilian, Andrzej
APPLICANT: Keese, Paul Konrad
TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE
TITLE OF INVENTION: USES THEREOF
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                                                                                                                                                                         DIDPVMFTEEYQVEYYQANHVVFDEFENFVGEQAWNFADFATSQGVMRVQGNKKGVFTRD
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                                                                                                                                                                                                                                   LIDVIALNRYNGWYFDGGDLEAAKVHLR---QEFHAWNKRCPGKPIMITEYGADTVAGFH
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                                                                                                                RKPKLAAHVFRERWINI
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                   Sequence 28, Application US/09270957
PATENT NO. 6641996
GENERAL INFORMATION:
APPLICANT: Richard A. Jefferson and Jorge E. M.
ATTLE OF INVENTION: MICROBIAL -GLUCUMONIDASE GI
TITLE OF INVENTION: PRODUCTS, AND USES THEREOF
FILE REFERENCE: 190106.405C1
      CURRENT APPLICATION NUMBER: US/09/270,957
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APPLICANT: Richard A. Jefferson and Jorge E. Mayer TITLE OF INVENTION: MICROBIAL -GLUCURONIDASE GENES, GE TITLE DE INVENTION: PRODUCTS, AND USES THEREOF FILE REFERENCE: 190106.405C1
CURRENT APPLICATION NUMBER: US/09/270,957
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 112
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
SEQ ID NO 18
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-270-957-18
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                          HPSVIMMSVANEPESNHPDAEGFFKALYETANEMD-RTRPVVMVSMMDAPDERTRDVALK 430
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                             RQPKLVAHVLRRLWSEV
                                                                                                    DIDPVMFTEEYQVEYYQANHVVFDEFENFVGEQAWNFADFATSQGVMRVQGNKKGVFTRD
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RKPKLAAHVFRERWTNI
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Pred. No. 5.7e-73;
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RESULT 11
US-09-862-660-2
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NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 28
LENGTH: 615
                                                                                                                                                                            Sequence 2, Application US/09862660 Patent No. 6664097 GENERAL INFORMATION:
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Best Local Similarity
Matches 220; Conser
           APPLICANT: RUBBELL, William
APPLICANT: Klaenhammer, Todd
TITLE OF INVENTION: LACTOBACILLUS BETA-GLUCURONIDASE AND DNA ENCODING THE
FILE REFERENCE: 5051.514
CURRENT APPLICATION NUMBER: US/09/862,660
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/206,372
PRIOR APPLICATION NUMBER: 60/206,372
PRIOR FILING DATE: 2000-05-23
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.0
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ORGANISM: Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                           YDPPQMFSEEYQAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVFTRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIDVIALNRYNGWYFDGGDLEAAKVHLR---QEFHAWNKRCPGKPIMITEYGADTVAGFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VASTEGLSGNVEIPNVILWEPLNTYLYQIKVELVNDGLTIDVYEEPFGVRTVEVNDGKFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTSNRFVEGEFILENARFWSLEDPYLYPLKVELEKDEYTLDI-----GIRTISWDEKRLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPVKIYTTPFTYVEDISVVTDFNGP---TGTVTYTVDFQ----GKAETVKVSVVDEEGKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GMNRVTVAVDNIL-----DDSTLPVGLYSERHEEGLGKVIRNKPNFDFFNYAGLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENELRYVVENRLKVGGFPSKVPDSGTHTVGFFGS-----FPPANFDFFPYGGII 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYVWYEREFTVPAYLKDQRIVLRFGSATHKAIVYVNGELVVEHKGGFLPFEAEINNSLRD
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GENERAL INFORMATION:
APPLICANT: Podsakoff, Gregory
APPLICANT: Podsakoff, Gordon
APPLICANT: Couto, Linda B.
APPLICANT: Yang, Bin
TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIA;
TITLE OF INVENTION: TREATMENT OF LYSOSOMAL DI
PILE REFERENCE: 0800-0021
CURRENT APPLICATION NUMBER: US/09/715,858
CURRENT FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SEQ ID NO 2
; LENCTH: 598
; TYPE: PRT
; ORGANISM: Lactobacillus gasseri
US-09-862-660-2
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US-09-715-858-4
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Best Local Similarity
Matches 207; Conserv
SOFTWARE:
SEQ ID NO 4
                                                                                                                                                                                                                                         Sequence 4, Application US/09715858 Patent No. 6582692
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                  PatentIn Ver. 2.0
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                                                                                                                              RECOMBINANT ADENO-ASSOCIATED VIRUS
                                                                                                             DISORDERS
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US-09-118-276-12
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                                                                                                                                                                                                                                                     Sequence 12, Application US/09118276 Patent No. 6693185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                      GENERAL INFORMATION:

APPLICANT: BABIYCHUK, BLENA;

APPLICANT: KUSHNIR, SERGEI;

APPLICANT: DE BLOCK, MARC;

APPLICANT: DE BLOCK, MARC;

APPLICANT: INZE, DIRK

TITLE OF INVENTION: METHODS AND MEANS TO MODULATE PROGRAMMED

TITLE OF INVENTION: CELL DEATH IN EUKARYOTIC CELLS

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Mus musculus
 COMPUTER READABLE FORM:
           STREET: 8180 G
CITY: MCLEAN,
STATE: VIRGINI
COUNTRY: USA
ZIP: 22102
                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315 YYTLPIGIRTVAVTKSKFLINGKPFYFQGVNKHEDSDIRGKGFDWPLLVKDFNLLRWLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 EYTLDIGIRTISWDEKRLYLNGKPVFLKGFGKHEEFPVLGQGTFYPLMIKDFNLLKWINA 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 YQDLCYEE--GPFTYKTTFYVPKXLSQ---KHIRLYFAAVNTDCEVFLNGEKVGENHIEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                  DATAGIHYDPPQMFSEEYQAELVEKTIRLL--LKKDYIIGTHVWAFADFKTPQNVRRPIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSFRTSHYPYSEBVLQLCDRYGIVVIDECPGVGIVLPQSFGNESLRHHL-----EVMEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDERTRDVALKYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHRKPIFVTEFGA
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                                              VIRGINIA
                                                                           E: SIXBEY, FRIEDMAN, LEEDOM,
8180 GREENSBORO DRIVE, SUITE
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                                                                           & FERGUSON
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; TYPE: AMINO ACID
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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ATTORNEY AGENT INFORMATION:

NAME: SCHULMAN, ROBERT M.; SALEN, KENNETH
REGISTRATION NUMBER: 31,196; 43,077
REFERENCE/DOCKET NUMBER: 6201-0003
TELECOMMUNICATION INFORMATION:
TELECHONE: (703) 790-9110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   695 FYFTGFGRHEDADLRGKGFDNVLMVHDHALMDWIGANSYRTSHYPYAEEMLDWADEHGIV
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                                                                                                                                                                                                                                                                                    WSIANEPDTRPQGAREYFAPLAEATRKLDPTRPITCVNVMFCDAHTDTISDL----FDVL
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                                                    EYQAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVFTRDRQPKLVAHV 555
                                                                                                                                                                                 WSVANEPESNHPDAEGFFKALYETANEMDRTRPVVMVSMM--DAPDERTRDVALKYFDIV 435
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EYQCAWLDMYHRVFDRVSAVVGEQVWNFADFATSQGILRVGGNKKGIFTRDRKFKSAAFL
                                                                                                                                            CLNRYYGWYVQSGDLETAEKVLEKELLAWQEKLHQPIIITEYGVDTLAGLHSMYTDMWSE
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FILE REFERENCE: 190106.405

CURRENT APPLICATION NUMBER: US/09/149,727

CURRENT FILING DATE: 1998-09-08

EARLIER APPLICATION NUMBER: US 60/058,263

EARLIER FILING DATE: 1997-09-09

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 6

LENGTH: 603

TYPE: PRT

ORGANISM: Escherichia coli

US-09-149-727-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09149727 Patent No. 6391547 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 205; Conserv
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APPLICANT: Kilian, Andrzej
APPLICANT: Keese, Paul Konrad
TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND
TITLE OF INVENTION: USES THEREOF
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LQKRWT 589
                                                                                                                                   CLNRYYGWYVQSGDLETAEKVLEKELLAWQEKLHQPIIITEYGVDTLAGLHSMYTDMWSE
                                                                                                                                                                  CVNRYYGWYIYQGRIEEGLQALEKDIEELYARHRKPIFVTEFGADAIAGIHYDPPQMFSE
                                                                                                                                                                                                                                   WSVANEPESNHPDAEGFFKALYETANEMDRTRPVVMVSMM--DAPDERTRDVALKYFDIV
                                                                                                                                                                                                                                                                                                  VIDEAPHVGI------TRYHYNPETQKIAEDNIRRMIDRHKNHPSVIM
                                                                                                                                                                                                                                                                                                                                           FYFTGFGRHEDADLRGKGFDNVLMVHDHALMDWIGANSYRTSHYPYAEEMLDWADEHGIV
                                                                                                                                                                                                                                                                                                                                                             QGTSGTLQVVNPHLWQPGEGYLYELCVTAKSQTECDIYPLRVGIRSVAVKGEQFLINHKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VMLYTTPNTWVDDITVVTHVAQ----DCNHASVDWQV----VANGDVSVELRDADQQVVATG
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                                LRRLWS 561
                                                                 EYQCAWLDMYHRVFDRVSAVVGEQVWNFADFATSQG1LRVGGNKKG1FTRDRKPKSAAFL
                                                                                                                                                                                                   WSIANEPDTRPQGAREYFAPLAEATRKLDPTRPITCVNVMFCDAHTDTISDL----FDVL
                                                                                                                                                                                                                                                                       VIDETAAVGFNLSLGIGFEAGNKPKELYSEEAVNGETQQAHLQAIKELIARDKNHPSVVM
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                                                                                                EYQAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVFTRDRQPKLVAHV
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RESULT 15 US-09-270-957-17

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; Sequence 17, Application US/09270957
; Patent NO. 6641996
; GENERAL INFORMATION:
; APPLICANT: RICHARD A. JEFFERSON and JOZGE E. MAYER
; TITLE OF INVENTION: MICROBIAL -GLUCURONIDASE GENES, GE
; TITLE OF INVENTION: PRODUCTS, AND USES THEREOF
; FILE REFERENCE: 190106.405C1
; CURRENT APPLICATION NUMBER: US/09/270,957
; CURRENT APPLICATION NUMBER: US/09/270,957
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FRSESEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 603
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; ORGANISM: Escherichia
US-09-270-957-17
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Post-processing: Minimum Match 0%
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seq length: 2000000000
Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

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24: /cgn2_6/ptodata/1/pubpaa/US10R_PUB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

11 9 11 11	- u u u 4	Result No.
1011 929 929 929 929 929 929	2999 2999 2999 2999	Score
33.7 31.0 31.0 31.0 31.0	99.9	Query Match
602 602 602 602 818	563 563 563	Length
18 15 15 14 14	155	DB
US-10-757-093-19 US-10-120-145-2 US-10-364-649-2 US-10-364-649-8 US-10-364-649-15 US-10-757-093-23 US-10-120-145-4	US-10-364-649-6 US-10-364-649-21 US-10-364-649-21 US-10-369-493-2995 US-10-757-093-20	SUMMARIES
Sequence 19, Appli Sequence 2, Appli Sequence 2, Appli Sequence 8, Appli Sequence 15, Appli Sequence 23, Appl Sequence 4, Appli	Sequence 6, Appli Sequence 21, Appl Sequence 2995, Ap Sequence 20, Appl	Description

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-10-195-518-5	-10-763	-09-893-525-4	-10-763-380-	9-893-525-	-10-763-	9-893-	-10-632-815-	-10-799-326-	-10-356-088-	-11-006-076-	0-757-	-10-161-408-	-10-369-493-	-10-364-649-	-10-364-	-10-120-145-	-10-161-403-10	-10-705	09-118-276-1	-10-757-093-	-10-757-093-	-10-757-093-1	-10-757-093-	-10-421-175-	-10-757-093-	-10-757-093-1	-10-757-093-	-10-673-93	-862-660-	0-757-093-	-649-2	US-10-364-649-18	-TU-12U-145-
ιn	42,	42,	e 40,	e 40,	æ	37,		28,	28,	e 106,	22,		842, Ap	23,	17, Āpp	6, Appl	106, Ap	e 12,	12,	4	16,	e 14,	15,		13,	e 12,	equence 21,	e 2,	e 2,	e 2,	e 28,	Sequence 18, Appl	е е,

ALIGNMENTS

US-10-364-649-6

Sequence 6, Application US/10364649

Sequence 6, Application VS/2030229921A1

GENERAL INFORMATION:
APPLICANT: RICHARD A. Jefferson and Jorge E. Mayer
TITLE OF INVENTION: MICROBIAL B-GLUCURONIDASE GENES,
TITLE OF INVENTION: PRODUCTS,
CURRENT APPLICATION NUMBER: US/10/364,649

FILER REFERENCE: 190106.4051

CURRENT FILING DATE: 2003-02-12

PRIOR APPLICATION NUMBER: US/970,957

PRIOR FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 112

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 6

SEQ ID N

S Query Match 99.9%; Score 2999; DB 15; Length 563; Best Local Similarity 100.0%; Pred. No. 1.9e-241; Matches 563; Conservative 0; Mismatches 0; Indels 0

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Gaps

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Sequence 21, Application US/10364649

Publication No. US20030229921A1

GENERAL INFORMATION:

APPLICANT: RICHARTA A. Jefferson and Jorge E. Mayer

ITILE OF INVENTION: MICROBIAL B-GLUCURONIDASE GENES, G

TITLE OF INVENTION: MICROBIAL B-GLUCURONIDASE GENES, G

TITLE OF INVENTION: PRODUCTS, AND USES THEREOF

FILE REFERRICE: 190106.405C1

CURRENT APPLICATION NUMBER: US/10/364,649

CURRENT FILING DATE: 2003-02-12

PRIOR APPLICATION NUMBER: US/964,649

PRIOR FILING DATE: 2003-02-12

PRIOR PRILING DATE: 2003-02-12

PRIOR PRILING DATE: 1909-03-17

NUMBER OF SEG ID NOS: 112

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NOS: 11

LENGTH: 563

TYPE: PRT

CORGANISM: Thermotoga maritima
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NAME/KEY: VARIANT
LOCATION: (1)...(563)
OTHER INFORMATION: Xaa =
15-10-364-649-21
                                                       Query Match
Best Local Sin
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                                                       99.9%; Score 2999; DB 15; Length ilarity 100.0%; Pred. No. 1.9e-241; Conservative 0; Mismatches 0; Indels
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
ITITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 2995
LENGTH: 563
TYPE: PRT
ORGANISM: Thermotoga maritima
US-10-369-493-2995
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; Sequence 2995, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
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Pred. No. 1.9e-241;
0; Mismatches 1;
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RESULT 4

US-10-757-093-20

US-10-757-093-20

Sequence 20, Application US/10757093

Publication No. US20050153448A1

GENERAL INFORMATION:
APPLICANT: CAMBIA

TITLE OF INVENTION: Fungal beta-glucuronidase gen
FILE REFERENCE: 415

CURRENT APPLICATION NUMBER: US/10/757,093

CURRENT APPLICATION NUMBER: US/10/757,093

CURRENT APPLING DATE: 2004-01-14

NUMBER OF SEQ ID NOS: 37

SOFTWARE: Patentin version 3.2

SEQ ID NO 20

LENGTH: 563

TYPE: PRT

ORGANISM: Thermotoga maritima
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Best Local Similarity
Matches 562; Conserv
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LYPLKVELEKDEYTLDIGIRTISMDEKRLYLNGKPVFLKGFGKHEEFPVLGQGTFYPLMI
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Pred. No. 1.9e-241;
0; Mismatches 1;
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Publication No. US20050153448A1
GENERAL INFORMATION:
APPLICANT: CAMBIA
TITLE OF INVENTION: Fungal beta-glucuronidas
FILE REFERENCE: 415
CURRENT APPLICATION NUMBER: US/10/757,093
CURRENT FILING DATE: 2004-01-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.2
SEQ ID NO 19
LENGTH: 570
TYPE: PRT
OPCANITION: Colfolbus Colfol
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                                                           GITRYHYNPETQKI-----AEDNIRRMIDRHKNHPSVIMWSVANEPESNHPDAEGF
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                            NISRVMSQEEIAKMFGDVKYFEKVRDTIKEMIRQHKNRPSVIMYSVMNEPPSDIREVAEF
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GENERAL INFORMATION:

APPLICANT: Jefferson, Andrzej
APPLICANT: Kilian, Andrzej
APPLICANT: Keese, Paul Konrad
ITILE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND ITILE OF INVENTION: USES THEREOF
FILE REFERENCE: 19016.405
CURRENT APPLICATION NUMBER: US/10/120,145
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/149,727
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/149,727
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,263
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN Ver. 2.0
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; TYPE: PRT
; ORGANISM: Bacillus
US-10-120-145-2
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US-10-120-145-2
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Publication No. US20030157684A1
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                                                                   LADREGLVVIDETPAVGV---HLNFMATTGLGEGSERVSTWEKIRTFEHHQDVLRELVSR
                                                                                                       LADRIGILVIDEAPHYGITRYHYN------PETQKIA----EDNIRRMIDR
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                                                                                                                                                                                                                                                  KKIRTSNRFVEGEFILENARFWSLEDPYLYPLKVELEKDEYTLDI-----GIRTISWDEK 267
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US-10-364-649-2
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 112
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TYPE: PRT
ORGANISM: Bacillus
                   369 HKNHPSVIMWSVANEPESNHPDAEGFFKALYETANEMD-RTRPVVMVSMMDAPDERTRDV 427
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DKNHPSVVMWSIANEAATEEEGAYEYFKPLVELTKELDPQKRPVTIVLFVMATPE--TDK
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Sequence 8, Application US/10364649

Publication No. US20030229921A1

GENERAL INFORMATION:
APPLICANT: Richard A. Jefferson and Jorge E. Mayer
TITLE OF INVENTION: MICROBIAL B-GLUCURONIDASE GENES, GENE
TITLE OF INVENTION: PRODUCTS, AND USES THEREOF
FILE REFERENCE: 190106.405C1
CURRENT APPLICATION NUMBER: US/10/364,649
CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: 10/364,649
PRIOR FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: US/9/270,957
PRIOR FILING DATE: 1909-03-17
NUMBER OF SEG ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8
LENGTH: 602
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; ORGANISM: Bacillus
US-10-364-649-8
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US-10-364-649-8
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Best Local Similarity
Matches 221; Conserv
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     ALKYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHR----KPIFVTEFGADAIA
                                                        DKNHPSVVMWSIANEAATEEEGAYEYFKPLVELTKELDPQKRPVTIVLFVMATPE--TDK
                                                                                                                                                           LADREGLVVIDETPAVGV---HLNFMATTGLGEGSERVSTWEKIRTFEHHQDVLRELVSR
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Publication No. US20030229921A1

GENERAL INFORMATION:
APPLICANT: Richard A. Jefferson and Jorge E. Mayer
ITITLE OF INVENTION: MICROBIAL B-GLUCURONIDASE GENES, C
ITITLE OF INVENTION: PRODUCTS, AND USES THEREOF
ILE REFERENCE: 190106.405C1
CURRENT APPLICATION NUMBER: US/10/364,649
CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: US/46,649
PRIOR APPLICATION NUMBER: US/964,649
PRIOR APPLICATION NUMBER: US/970,957
PRIOR FILING DATE: 2003-02-12
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15
LENGTH: 602
TYBE: PRT
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US-10-364-649-15
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31.0%; Score 929; DB 15;
Best Local Similarity 35.6%; Pred. No. 1.7e-68;
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428 ALKYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHR-----KPIFVTEFGADAIA 483
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                                                                                                                                HKNHPSVIMWSVANEPESNHPDAEGFFKALYETANEMD-RTRPVVMVSMMDAPDERTRDV 427
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                                                                                                                                                                                 LADREGLVVIDETPAVGV---HLNFMATTGLGEGSERVSTWEKIRTFEHHODVLRELVSR
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                                                                                DKNHPSVVMWSIANEAATEEEGAYEYFKPLVELTKELDPQKRPVTIVLFVMATPE--TDK
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Sequence 23, Application US/10757093

Publication No. US20050153448A1

GENERAL INFORMATION:
APPLICANT: CAMBIA

FILE REFERENCE: 415

CURRENT APPLICATION NUMBER: US/10/757,093

CURRENT FILING DATE: 2004-01-14

NUMBER OF SEQ ID NOS: 37

SOFTWARE: Patentin version 3.2

FEQ ID NO 23

LENGTH: 602

TYPE: PAT

ORGANISM: Staphylococcus sp.
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US-10-757-093-23
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Best Local Similarity
Matches 221; Conserv
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                     GFHDIDPVMFTEEYQVEYYQANHVVFDEFENFVGEQAWNFADFATSQGVMRVQGNKKGVF
                                                        GIHYDPPQMFSEEYQAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVF 543
                                                                                                                                             ALKYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHR----KPIFVTEFGADAIA 483
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APPLICANT: Kélferson, Richard A.
APPLICANT: Kélferson, Richard
APPLICANT: Kélferson, Richard
APPLICANT: Kélferson, Richard
APPLICANT: Kélferson
ITILE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GEN
ITILE OF INVENTION: WICROBIAL BETA-GLUCURONIDASE GENES, GEN
ITILE OF INVENTION: WIGHES THEREOF
FILE REFERENCE: 190106.405
CURRENT APPLICATION UNUMBER: US/10/120,145
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/14
PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 71
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 618
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US-10-120-145-4
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Matches
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Publication No. US20030157684A1
GENERAL INFORMATION:
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ORGANISM: Bacillus
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                            GIHYDPPQMFSEEYQAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVF
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GFHDIDPVMFTEEYQVEYYQANHVVFDEFENFVGEQAWNFADFATSQGVMRVQGNKKGVF
                                                                              VAELIDVIALNRYNGWYFDGGDLEAAKVHLR---QEFHAWNKRCPGKPIMITEYGADTVA
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                                                                                                                                                                                                                                                                                                                                    KFLINNKPFYFKGFGKHEDTPINGRGFNEASNVMDFNILKWIGANSFRTAHYPYSEELMR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIIRPVLIEFTDHARILDIWVDTSESEPEKKLGKVKVKIEVSEEAVGQEMTIKLG--EEE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRDGMNRVTVAVDNIL------DDSTLPVGLYSERHEEGLGKVIRNKPNFDFFNYA
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                                                                                                        ALKYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHR----KPIFVTEFGADAIA 483
                                                                                                                                                                 DKNHPSVVMWSIANEAATEEEGAYEYFKPLVELTKELDPQKRPVTIVLFVMATPE--TDK
                                                                                                                                                                                                        HKNHPSVIMMSVANEPESNHPDAEGFFKALYETANEMD-RTRPVVMVSMMDAPDERTRDV
                                                                                                                                                                                                                                                                                           LADRLGILVIDEAPHVGITRYHYN------PETQKIA-----EDNIRRMIDR
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US-10-120-145-8
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US-10-120-145-8
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CURRENT FILING DATE: 2002-04-11

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/149,727

PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,263

PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-09

NUMBER OF SEQ ID NOS: 71

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 8

LENGTH: 607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 30.8%; Score 925; DB 14; Best Local Similarity 35.7%; Pred. No. 3.6e-68; Matches 220; Conservative 92; Mismatches 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jefferson, Richard A.
APPLICANT: Kilian, Andrzej
APPLICANT: Keese, Paul Konzad
TITLE OF INVENTION: MICHOSIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 190106,405
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YDPPQMPSEEYQAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVFTRD
                                                                LIDVIALNRYNGWYFDGGDLEAAKVHLR---QEFHAWNKRCPGKPIMITEYGADTVAGFH
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                                                                                                     YFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHR----KPIFVTEFGADAIAGIH
                                                                                                                                              HPSVVMWSIANEAATEEEGAYEYFKPLVELTKELDPQKRPVTIVLFVMATPE--TDKVAE
                                                                                                                                                                                    HPSVIMWSVANEPESNHPDAEGFFKALYETANEMD-RTRPVVMVSMMDAPDERTRDVALK 430
                                                                                                                                                                                                                             REGLVVIDETPAVGV---HLNFMATTGLGEGSERVSTWEKIRTFEHHODVLRELVSRDKN
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FILE REFERENCE: 190106.405C1
CURRENT APPLICATION NUMBER: US/10/364,649
CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: 10/364,649
PRIOR FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: US 09/270,957
PRIOR FILING DATE: 199-03-17
NUMBER OF SEQ ID NOS: 112
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
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US-10-364-649-18
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Best Local Similarity
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TITLE OF INVENTION: MICROBIAL B-GLUCURONIDASE GENE-
TITLE OF INVENTION: PRODUCTS, AND USES THEREOF
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ORGANISM: Bacillus
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DIDPVMFTEEYQVEYYQANHVVFDEFENFVGEQAWNFADFATSQGVMRVQGNKKGVFTRD
                                                                                                      YFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHR----KPIFVTEFGADAIAGIH
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                                       YDPPOMESEEYOAELVEKTIRLLLKKDYIIGTHVWAFADFKTPONVRRPILNHKGVFTRD
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Sequence 28, Application US/10364649

Publication No. US20030229921A1

GENERAL INFORMATION:

APPLICANT: Richard A. Jefferson and Jorge E. Mayer

ITILE OF INVENTION: MICROBIAL B-GLUCURONIDASE GENES, G

TITLE OF INVENTION: MICROBIAL B-GLUCURONIDASE GENES, G

TITLE REFERENCE: 190106.405C1

CURRENT APPLICATION NUMBER: US/10/364,649

CURRENT FILING DATE: 2003-02-12

PRIOR APPLICATION NUMBER: US/94,649

PRIOR FILING DATE: 2003-02-12

PRIOR PILING DATE: 2003-02-12

PRIOR PILING DATE: 1909-03-17

NUMBER OF SEQ ID NOS: 112

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 28

LENGTH: 615

TYPE: PRT

CORGANISM: Bacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-10-364-649-28
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Best Local Similarity
Matches 220; Conserv
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                     DIDPVMFTEEYQVEYYQANHVVFDEFENFVGEQAWNFADFATSQGVMRVQGNKKGVFTRD
                                                                                                                                 YFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHR----KPIFVTEFGADAIAGIH
                                                                                                                                                                                                                           HPSVIMWSVANEPESNHPDAEGFFKALYETANEMD-RTRPVVMVSMMDAPDERTRDVALK
                                                                                                                                                                                                                                                                                                         RLGILVIDEAPHVGITRYHYN------PETQKIA-----EDNIRRMIDRHKN
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                                                   YDPPQMFSEEYQAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVFTRD
                                                                                                                                                                                  HPSVVMWSIANEAATEEEGAYEYFKPLVELTKELDPQKRPVTIVLFVMATPE--TDKVAE
                                                                                                                                                                                                                                                                                                                                                                                                                                   VASTEGLSGNVEIPNVILWEPLNTYLYQIKVELVNDGLTIDVYEEPFGVRTVEVNDGKFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GMNRVTVAVDNIL------DDSTLPVGLYSERHEEGLGKVIRNKPNFDFFNYAGLH
                                                                                                                                                                                                                                                                   REGLVVIDETPAVGV---HLNFMATTGLGEGSERVSTWEKIRTFEHHODVLRELVSRDKN
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; LENGTH: 641
; TYPE: PRT
; ORGANISM: Scopulariopsis sp. isolate RP38.3
US-10-757-093-2
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US-10-757-093-2
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Publication No. US20050153448A1
GENERAL INFORMATION:
APPLICANT: CAMBIA
TITLE OF INVENTION: Fungal beta-glucuronidase
FILE REFERENCE: 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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CURRENT FILLING DATE: 2004-01-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.2
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les 219; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 LKPQANAIRELLSLDGTWNFALPQSREIEEDQGWTSVIPPKLQIPVPASYNDIFTDPAIR 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VRPQRNKKRFILILNGVWNLEV-----TSKDRP---IAVPGSWNEQYQDLCYE
                                                                                                                                        HAVDEVLMSEEYQINLLRMSHKVFDSIDSIVGEHVMNFADFQTPHTGVNRVDGNKKGVFT
                                                                                                                                                                 HYDPPQMFSEEYQAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQ-NVRRPILNHKGVFT
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                                                                                                 RDROPKLVAHVLRRLW 560
                                                                                                                                                                                                                           CLISDLFDFLSLNRYYGWYVQTGDLESAEVAMEEELLQWVDEYDKPIIMSEYGADTLAGL
                                                                                                                                                                                                                                                    AL--KYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHRKPIFVTEFGADAIAGI 485
                                                                                                                                                                                                                                                                                                         RDKNHASVVSWCVTNEPASAEDGAREYFQPLVELTRELDPTRPVTFTNVMGA----TVDK
                                                                                                                                                                                                                                                                                                                                                                                          VMEYADRHGIVVIDEVAAVGLNLGISAGLRGDEPPKTFTEDKVNNETQKTHAQALRELIH
                                                                                                                                                                                                                                                                                                                                                                                                                                 WLDLADRLGILVIDEAPHVGI------TRYHYNPETQKIAEDNIRRMID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E--GPFTYKTTFYVPKXLSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEVDVTGK 104
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                                                             RERRPKAAAHELKRRW
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                                                             626
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Maximum DB seq length: 200000000
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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1: gb_ba:*

2: gb_htg

3: gb_in

4: gb_or

5: gb_or

6: gb_f

7: gb_
9: gt

10: gt
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Match Length DB
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        4708233 seqs, 24227607955 residues
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1689
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Copyright (c) 1993 - 2005 Compugen Ltd.
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HUMGLCB
AX147652
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AR428149 Sequence
AB001766 Thermotog
AF012421 Felis cat
AF012424 Felis cat
AF012795 Canis fam
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BT010073 Drosophil
AR344264 Sequence
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CQ847932 Sequence
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Y00717 Rat mRNA foo
AX827491 Sequence
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115.6 114 114	138.6 138.6 130.4 127.6 123.6 123.6 123.6	159.6 159.6 157.8 154.8 142.2 142.2 141.4 141.4 141.4 141.4 141.4 141.4	159.6
6.8 6.7 6.7			9.4
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ALIGNMENTS

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CDS	1261 GACGAGAGAACAAGAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTAC 1320 	B &
gene	1201 ACTGCCAATGAAATGGATCGAACACGCCCCGTTGTCATGGTGAGCATGATGGACGCACCA 1260 	B &
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AUTHORS	1021 CCGCACGTTGGTATCACAAGGTACCACTACAATCCCGAGACTCAGAAGATAGCAGAAGAC 1080 	문왕
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ORGANISM REFERENCE	781 ACGATCAGCTGGGACGAGAAGAGGCTCTATCTGAACGGGAAACCTGTCTTTTTGAAGGGC 840	음 성
VERSION KEYWORDS SOURCE	CTTTATCCTCTCAAGGTGGAACTTGAAAAAGACGAGTACACTCTGGACATCGGAATCAGA	Db 45
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RESULT 2 AE001766/c	661 TTCGTCGAAGGGGAGTTCATCCTCGAAAACGCCAGGTTCTGGAGCCTCGAAGATCCATAT 720	Ş
Db 168	601 GGACAGGAGATGACGATCAAACTTGGAGAGGAAAAAAAAA	dg Vo
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Dy 163	541 GAACCGGAGAAGAACTTGGAAAAGTGAAAGTGAAGATAGAAGTCTCAGAAGAAGAGGCGGTG 600	Ş
		Db ·
Оу 15	CTGATAGAGTTCACAGACCACGCGAGGATACTCGACATCTGGGTGGACACGAGTGAGT	Ş
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		₽
Db 14	361 AAAGTGGGAGGATTTCCCTCGAAAGGTTCCAGACAGCGGGACTCACACCCGTGGGATTTTTTT 420	γ
	01 GTGACGGGAAAGTGAAATCCGGAGAGAACGAACTCAGGGTGGTTGTTGAGAACAGATTG	д :
Оу 131	01 GTGACGGGGAAAGTGAAATCCGGAGAAACGAACTCAGGGTGGTTGTTGAGAACAGATTG	\$ {
Db 13:		묽

gene	REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE	ORS ORS	77 66 7
DNA" 274" B:AE000666 p nce similari	2 (bases 1 to 12583) Relson, K.E., Clayton, R.A., Gill Haft, D.H., Hickey, E.K., Peterso McDonald, L., Utterback, T.R., Ma Stewart, A.M., Cotton, M.D., Prat Richardson, D., Heidelberg, J., S White, O., Salzberg, S.L., Smith, Direct Submission Submitted (01-JUN-1999) The Ins Medical Center Dr, Rockville, M Medical Center Dr, Rockville, M Location/Qualifiers 1. 12583 /organism="Thermotoga"	AE001766 AE001512 AE001766 AE000512 AE001766 AE000512 AE001766 AE000512 AE001766.1 GI:4981600 Thermotoga maritima MSB8 M Thermotoga maritima MSB8 M Thermotoga maritima MSB8 Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga. 1 (bases 1 to 12583) Nelson, K.E., Clayton, R.A., Gill, S.R., Gwinn, M.L., Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Nelson, W.C., Ketchum, K.A., McDonald, L., Utterback, T.R., Malek, J.A., Linher, K.D., Garrett, M.M., Stewart, A.M., Cotton, M.D., Pratt, M.S., Phillips, C.A., Richardson, D., Heidelberg, J., Sutton, G.G., Fleischmann, R.D., Richardson, D., Heidelberg, J., Smith, H.O., Venter, J.C. and Fraser, C.M. Eisen, J.A., White, O., Salzberg, S.L., Smith, H.O., Venter, J.C. and Fraser, C.M. Evidence for lateral gene transfer between Archaea and bacteria Nature 399 (6734), 323-329 (1999) 10166671	321 TACGGCTGGTACATCTATCAGGGAAGGATAGAAGAAGGACTTCAAGCTCTGGAAAAAGAC 1380 381 ATAGAAGAGCTCTATGCAAGGCACAGAAAGCCCATCTTTGTCACAGAATTCGGTGCGGAC 1440 381 ATAGAAGAGCTCTATGCAAGGCACAGAAAGCCCATCTTTGTCACAGAATTCGGTGCGGAC 1440 381 ATAGAAGAGCTCTATGCAAGGCACAGAAAAGCCCAATCTTTTTCACAGAATTCGGTGCCGAC 1440 381 ATAGAAGAGCTCTATGCAAGCCCACAGAAAGCCCAATTCTTCCCGAAGAATTCGGTGCCGAC 1440 381 ATAGAAGAGCTCACTACAGATCCACCTCAAATGTTCTCCCGAAGAATTCGGTGCCGAC 1500 441 GCGATAGCTGGCATCCACTACGATCCACCTCCAAATGTTCTCCCGAAGAGTACCAAGCAGAG 1500 501 CTCGTTGAAAAGAAGACGATCAGCTCCTTTTGAAAAAAAGACTACATCATCGGAACAACACACGTG 1560 501 CTCGTTGAAAAGAACGATCAGGCTCCTTTTGAAAAAAAGACTACATCATCGGAACACACAC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (1650...1913)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEALTYQFAEKLSRRGIRVPDIAIAGGFSTEDGVLKAIAMGSPYVKAVCMGRALMIPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:862985 GB:AL009126 percent
by sequence similarity;
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/protein_id="AD36138.1"
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/GLVGESGCGKTTTAKLIMRGIEPTEGEIVLNMDGEKVDITKLSEKELREKGVRRFLQM
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complement (6284. .7309)
                                                                                                                                                                                                                                                                                                    /product="oligopeptide ABC transporter, permease protein"
/protein_id="AAD36140.1"
/db_xref="GI:4981606"
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/transl_table=11
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/transl_table=11
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/transl_table=11
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/db_xref="GI:4981609"
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/product="beta-glucuronidase"
'Locus_tag="TM1066"
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                                         .10403)
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/locus tag="TM1066"
/note="similar to SP:P42062
identity: 62.93; identified
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/transT_table=11
/product="0ligopeptide ABC
/protein_id="AAD36141.1"
/db_xref="GI:4981607"
                                                                                   CTCAAGGTGGAACTTGAAAAAGACGAGTACACTCTGGACATCGGAATCAGA
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Fyfe,J.C., Kurzhals,R.L., Lassaline,M.E., Henthorn,F
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Submitted (03-JUL-1997) Microbiology, Michigan
413 Giltner Hall, East Lansing, MI 48824, USA
Location/Qualifiers
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Direct Submission
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Qyhlvldokkreyvvgeliwngadfmtnosporvmgnkkgiftropppkgaafflirer
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/mol type="maNA"
/db_xref="taxon:9685"
/tissue_type="liver"
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/note="lysosomal hydrolase; lysosomal exooligosaccharidase in stepwise degradation of glucuronic acid-containing oligosaccharide sidechains of proteoglycans"
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/protein_id="AAD01498.1"
/db_xref="GI:4102551"
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CAACCAAAAGGGGCAGCGTTCCTTTTGCGA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; 1 (bases 1 to 2014) Fyfe, J.C., Kurzhals, R.L., Lassaline, M.E., Henthorn, P. Wang, P., Wolfe, J.H., Giger, U., Haskins, M.E., Patters Sun, H., Jain, S. and Yuhki, N. Molecular basis of feline beta-glucuronidase deficie model of mucopolysaccharidosis VII Genomics 58 (2), 121-128 (1999) Direct Submission Submitted (03-JUL-1997) Microbiology, 413 Giltner Hall, East Lansing, MI 488 Location/Qualifiers AF012424 2014 bp mRNA linear MAM 09-Felis catus cell-type fibroblast mutant beta-glucuronidase mRNA, GUSB-MPS VII mutant allele, complete cds. Fyfe, J.C., Kurzhals, R.L. (bases 1 to 2014) /organism="Felis catus"
/mol_type="mRNA"
/db_xref="taxon:9685" gene="GUSB" GI:4102552 type="fibroblast" and Henthorn, P.S. 48824, Michigan 1824, USA Henthorn, P.S., S., Patterson, D. deficiency: State University, Futeleostomi; Alur, P. an animal (GUSB)

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OLCDRYGIVVJDESPGYGIVLVESYSUVSLQHHLEVNEELVRDKNHPAYNVMGSVAE
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PLASCRITIA ALNNTLFPHTLPPGTILYQTDTSKYPKQYFVQNINFDFFYYAGLHRPVL
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/protein_id="AAD01499.1"
/db_xref="GI:4102553"
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Ray, J., Bouvet, A., DeSanto, C., Fyfe, J.C., Xu, D., Wolfe, J.H., Aguirre, G.D., Patterson, D.F., Haskins, M.E. and Henthorn, P.S. Cloning of the canine beta-glucuronidase cDNA, mutation identification in canine MPS VII, and retroviral vector-mediated correction of MPS VII cells Genomics 48 (2), 248-253 (1998)
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QYHLVLDQKRKEYVVGELIWNFADFMTDQSPQRAVGNRKGIFTRQRQPKAAAFLLREF
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/mol_type="mRNA"
/db_xref="taxon:9615"
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52.8%;
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Pred. No. 7.9e-40;
0; Mismatches 418;
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                          Matches 487;
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Best Local Similarity
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Human Genetics Unit, Crewe Road,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Cercopithecus.

1 (bases 1 to 2155)
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Vervoort R.
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TGGATCTTGCCGACAGACTCGGAATCCTTGTGATAGACGAAGCCCCGCACGTTGGTATCA 1036
                                                                                                                                                                                                                                                   AGAAGAGGCTCTATCTGAACGGGAAAACCTGTCTTTTTGAAGGGCTTTGGAAAGCACGAGG
                                                               TTCGCTGGCTTGGTGCCAATGCCTTCCGCACCACCACTACCCCTACGCCGAGGAAGTGC
                                                                                                                                           ATGCGGACATCCGAGGGAAGGGCTTCGACTGGCCGCTGCTGGTGAAGGACTTCAACCTGC
                                                                                                                                                                                   AATTCCCCGTTCTGGGGCAGGGCACCTTTATCCATTGATGATAAAAGACTTCAACCTTC
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                                                                                                   TGAAGTGGATCAACGCGAATTCTTTCAGGACCTCTCACTATCCTTACAGTGAAGAGTGGC
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ILDERWYQDLSTRVVLRIGSAHAYAI VWVNGVHTLEHEGGYLPEFADISNLVQVGPLS
SHVRITIAINTLTSSTLPEOGTIQYLTDISKYPKGYPF IQUTYPDFRVXAGLQRSVLLY
TTPTAYIDDITVTTGVEHDTGLVNYQISVKGSNLFELEVRLLDAENKLVANGTGIQQQ
LKVPGARLWRPYLMHERPAYLYSLEVRLTAQTSLGPVDFYTLVGIRTVAVTESQFL
IKKVPGARLWRPYLMHERPAYLYSLEVRLTAQTSLGPVDFYTLVGIRTVAVTESQFL
INGKPPYFHGVNKHBDDAIRGKGFDWPLLVKDFNLLRWLGANAFRTSHYPYABEVLQM
CDRYGIVVIDGCPGVGLALPQFFNNVSLQNHRKVMEEVVRRDKNHPAVVMWSVANEPA
SHLESBAGYYLKMVITHTKALDPSRPYTFVTNSNYADKGAPYUDICLNSYYSMYHDY
CHLETTOPDTWATUNGWYDI
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HVVLDQKRRKYVVGELIMNFADFMTEQSPTRVLGNKKGVFTRQRQPKSAAFLLRERYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to Homo sapiens beta-glucuronidase; beta-D-glucuronoside; glucuronosohydrolase; glucuronohydrolase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KIANETRYPHSIAKSQCLENSPFT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="beta-glucuronidase"
/protein_id="AAC34593.1"
/db_xref="GI:3549609"
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/mol_type="mRNA"
/db_xref="taxon:9534"
/cell_line="COS7"
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Pred. No. 1.5e-35;
0; Mismatches 436
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oad, Edinburgh EH4
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                                                                                                                                                                                                           Drosophila sp.
Drosophila sp.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                               Sequence 3461 from Patent WO0171042.
                                                                                                  Venter,J.C., Adams,M., Li,P.W. and Myers,E.W.
Detection kits, such as nucleic acid arrays, for detecting the expression of 10,000 or more Drosophila genes and uses thereof Patent: WO 0171042-A 3461 27-SEP-2001;
PE Corporation (NY) (US)
Location/Qualifiers
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/mol_type="unassigned
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RESULT 8 BC014142

DEFINITION FOCUS

BC014142 2182 Homo sapiens glucuronidase, b IMAGE:4662011), complete cds.

2182 bp ase, beta,

mRNA linear PRI 29-JUN-2004 mRNA (cDNA clone MGC:20659

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TCTTTACAAGGAACCGACAACCCCAAAGAAGTGGCTCACATTCTTAGGCGGCGGT
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                                                                                   CCTTTGCAGATTTTAAGACTCCTCAGAATGTGAGAAAGACCCATTCTCAACCACAAGGGTG
                                                                                                                              TCCACTACGATCCACCTCAAATGTTCTCCGAAGAGTACCAAGCAGAGCTCGT------
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                                                                                                                                                             -TGAAAAGACGATCAGGCTCCTTTTGAAAAAAGACTACATCATCGGAACACACGTGTGGG
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schhler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Wullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R. W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Schein, J.E., Jones, S.J. and Warra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 30 Row: o Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri nih.gov
Akhter,N., Ayele,K., Beckstrome-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,O.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
On Dec 19, 2003 this sequence version replace
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2182)
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BC014142.2
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/clone="MGC:20659 IMAGE:4662011"
/tissue type="Colon, adenocarcinoma"
/clone_Tis="NH MGC:15"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGACAAGGGGGCTCCGTATGTGGATGTGATCTGTTTGAACAGCTACTACTTCTTGGTATC 1526
                                                                                                                                                GAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTACTACGGCTGGTACA 1333
                                                                                                                                                                                                                                                              TGGATCGAACACGCCCCGTTGTCATGGTGAGCATGATGGACGCACCAGACGAGAGAACAA 1273
                                                                                                                                                                                                                                                                                                                            CGTCCCACCTAGAATCTGCTGGCTACTTGAAGATGGTGATCGCTCACACCAAATCCT 1418
                                                                                                                                                                                                                                                                                                                                                                                   AGTCCAACCATCCAGACGCGGAGGGTTTCTTCAAAGCCCCTTTATGAGACTGCCAATGAAA 1213
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FLPSRLRITIAINNTLTPTTLEPGTIQYLTDTSKYPKGYFQNTYFDFFRYAGLQRSV
LLYTTPTTYIDDITVTTSVEVQDDSGLVNYQISVKGSNLFKLEVRLLDAEMKVVANGTGT
QQLKVPGVSLWWPYLMHERPAYLYSLEVQLTAQTSLGPVSDFYTLPVGIRTVAVTKS
QPLINGKFYFHGVNKHEDADIRGKGFDWFLLVKDFNLLRWLGANAFRTSHYFYAEEV
MQMCDRYGIVVLDECPGYLALPQFFNNVSLHHMQVMESVAR
MQMCDRYGIVVLDCPGYLALPQFFNNVSLHHMQVMESVAR
EPASHLESAGYYLKMVIAHTKSLDPSRPVTFVSNSNYNAADKGAPYVDVLCLNSYYSMY
HDYGHLELIQLQLATQFENWYKKYQKFIIQSSYGAETIAGFHQDPPLMFTEEYQKSLL
HDYGHLELIQLQLATQFENWYKKYQKFIIQSSYGAETIAGFHQDPPLMFTEEYQKSLL
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wspradpsdwrrrgpeeqwyrrplwesgptvdmpvpssfndlsqdwrlrhfvgwvwye
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/protein_id="AAH14142.1"
/db_xref="GI:15559560"
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/note="synonym: MPS7"
/db_xref="LocusID:2990"
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Pred. No. 1.9e-35;
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JOURNAL
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                               gene
                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                           Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site
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Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J., Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J., Stapleton, M., Chawez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E., Champe, M., Chawez, C., Dorsett, V., Dresnek, D., Farfan, D., Li, P., Liao, G., George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G., George, R., Gonzalez, M., Guarin, H., Kronmiller, J., Paragas, V., Park, S., Miranda, A., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Man, K., Yu, C., Lewis, S.B., Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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Sequence submitted by:
Berkeley Drosophila Ge
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Drosophila melanogaster LD10588
                                                                                                                                                                                                             cdna@fruitfly.berkeley.edu.
Location/Qualifiers
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/db_xref="taxon:7227"
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0; Mismatches 435;
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                                                                           CAAGGTACCA---CTACAATCCCGAGACTCAGAAGATAGCAGAAGACAACATAAGAAGAA
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/mol_type="genomic
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0136603-A 1 25-MAY-2001;
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/mol_type="unassigned DN:
/db_xref="taxon:9606"
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TCACTCGGCAGAGACAACCAAAAAGTGCAGCGTTCCTTTTGCGA
                                                                    TTGCCGATTTCATGACTGAACAGTCACCGACGAGAGTGCTGGGGGAATAAAAAGGGGGATCT
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Mammalia; Eutheria;
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                                                                                          GAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTACTACGGCTGGTACA 1333
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ACGACTACGGGCACCTGGAGTTGATTCAGCTGCAGCTGGCCACCCAGTTTGAGAACTGGT
                                                                    CAGACAAGGGGGCTCCGTATGTGGATGTGATCTGTTTGAACAGCTACTACTCTTGGTATC 1551
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="M15182"
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                                                                                                                                                                                                                                                                                                    Original source text: Human fibroblasts cDNA clone pHUGF and placenta cDNA clones pHUGF13 and pHUGF15.

Draft entry and copy of computer-readable sequence of [1] kindly provided by R.D.Miller, 08-MAY-1987.

Four potential N-linked glycosylation sites are located at bases 543-551, 840-848, 1284-1292 and 1917-1925. Potential poly-A signals were found 25 and 48 bp upstream of the poly-A site at nucleotides 2139-2144 and 2162-2167 respectively.

Two types of mRNA exit due to alternative splicing. The short form, lacking bases 939-1091 below, encodes a protein lacking beta-glucuronidase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oshima,A., Kyle,J.W., Miller,R.D., Hoffmann,J.W., Powell,P.P., Grubb,J.H., Sly,W.S., Tropak,M., Guise,K.S. and Gravel,R.A. Cloning, sequencing, and expression of cDNA for human beta-glucuronidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alternative splicing; beta-D-glucuronoside glucuronosohydrolase; beta-glucuronidase; hydrolase
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                         /product="glucuronidase-b
27. .1982
/db_xref="GDB:G00-120-025"
/translation="MARGSAVAWAALGPLLWGCALGLQGGMLYPQESPSRECKELDGL
WSFRADFSDNRRRGFEEQWYRRPLWESGPTVDMPVPSSFNDISQDWRLRHFVGWVWYE
                                             /proteIn_id="AAA52561.1"
/db_xref="GI:183233"
                                                                                        /gene="GUSB"
/note="beta-glucuronidase
                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
                                                                             codon_
                                                                                                                                                     gene="GUSB"
                                                                                                                                                                                   gene="GUSB"
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PLPSRIAITIALWILTFTTLPFGTIQYLTDTSKYPKGYFVQNYYPFDEFNYAGLQRSV

LLYTFFTYLDDITVTTSVGODGSLVNYQISVGGSNLFKLEVRLLDARMXVVANGTGSV

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EQYHLGLIQKRRKYVVGELINWFADISMTEQSFTRVLGNKKGIFTRORQPKSAAFLLRE

RYWKIANETRYPHSVAKSQCLENSPFT"
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TCCACTACGATCCACCTCAAATGTTCTCCGAAGAGTACCAAGCAGAGCTCGTTGAAAAG- 1512
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                                                                           ATAAGAAGTATCAGAAGCCCATTATTCAGAGCGAGTATGGAGCAGAAACGATTGCAGGGT 1671
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93. .1979
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Direct Submission
Submitted (07-JAN-1988) Miller R.D., E.A.
Submitted (07-JAN-1988) Miller R.D., E.A.
Biochemistry, St. Louis University School
Grand Blvd., St. Louis, MO, 63104
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat liver beta-glucuronidase. cDNA cloning, and expression of a chimeric protein in COS Biochem. J. 250 (2), 547-555 (1988)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Powell, P.P., Kyle, J.W., Miller, R.D., Pantano, J., Grubb, J.H. and
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                                                                                            /product="beta-glucuronidase"
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/product="beta-glucuronidase precurs
/protein_id="CAA68705.1"
/db_xref="GOA: P06760"
/db_xref="GOA: P06760"
/db_xref="UniProt/Swiss-Prot: P06760"
                                                                                  TQCMGSRPFTF"
                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"

/mol_type="mRNA"

/strain="Sprague-Dawley"

/db xref="taxon:10116"

/clone="pRLGS"
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                           CAACCCAAACTCGTTGCTCATGTACTGAGA 1671
                                                                                                                                           TTGAA-----AAAAGACTACATCATCGGAACACACGTGTGGGCCTTTGCAGATTTTAAG
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AACCCCAAGATGGCAGCCTTCATTTTGCGA 1819
                                                          ACGAACCAGTCACCACTGAGAGTAACAGGAAACAAGAAGGGGGATCTTCACTCGACAGAGA
                                                                                     ACTCCTCAGAATGTGAGAAGACCCATTCTCAACCACAAGGGTGTTTTCACAAGAGACAGA 1641
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Pred. No. 1.6e-33;
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RESULT 15 AX827491 LOCUS

DEFINITION

AX827491 Sequence 225 from

Patent EP1344834.

2472 bp

DNA

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REFERENCE
AUTHORS
TITLE
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Best Local Similarity 51.3%;
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Patent:
F. HOFFM
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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AX827491.1
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                                                                                                                                                                                                                                                                                                          GACGCGGAGGGTTTCTTCAAAGCCCCTTTATGAGACTGCCAATGAAATGGATCGAACACGC 1227
                                                                                                                                                                                                                                                                                                                                                                       GCAAATTCCTTTCGTACCAGCCACTATCCCTACTCGGAGGAGGTACTTCAGCTCTGTGAC
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CCTCAAATGTTCTCCGAAGAGTACCAAGCAGAGCTCGTTGAAAAGACGATCAGGCTCCTT 1527
                                AAGCCAATTATCCAGAGCGAGTATGGAGCAGACGCCGTCTCGGGGGCTTCATGAGGATCCA
                                                             AAGCCCATCTTTGTCACAGAATTCGGTGCGGACGCGATAGCTGGCATCCACTACGATCCA 1467
                                                                                            CTGGAGGTGATTCAGCTGCAGCTGACTAGCCAGTTTGAGAACTGGTATAAGATGTACCAG
                                                                                                                          АТАGАAGAAGAAGGACTTCAAGCTCTGGAAAAAAGACATAGAAGAGCTCTATGCAAGGCACAGA 1407
                                                                                                                                                         CCGTACGTGGACGTGATTTGTGTGAACAGTTACTTATCCTGGTATCATGACTACGGGCAT
                                                                                                                                                                                                                        CCTGTGACCTTTGTGAGCAATA------CCAGATATGACGCAGACATGGGGGCC 1473
                                                                                                                                                                                                                                                     CCCGTTGTCATGGTGAGCATGATGGACGCACCAGACGAGAGAACAAGAGACGTGGCGCTG 1287
                                                                                                                                                                                                                                                                                     CCTGCCGGATATTACTTCAAGACGCTGATCGCCCACACCAAAGCCCCTGGACCCCACCCGT
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Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:10116"
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Search completed: September 2, 2005, 00:30:40 Job time: 7498 secs

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Acf57506 Human bet
Adj62864 Human bet
Adp10326 Reference
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Ads48252 Bacterial
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AAA07937;

AAA07937 standard; DNA; 1689

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ALIGNMENTS

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                                                                                                                          Novel microbial beta-glucuronidase genes and gene products used as reporter/effector molecule, as diagnostic tool, in positive selection, target molecules to specific cells and to detect and track linked genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                Microbial; beta-glucoronidase; GUS; Enterobacter; Salmonella; Pseudomonas; Staphylococcus; Thermotoga; transgenic plant; bioindicator; transgenic insect; marker; glucuronide detoxification; ds.
                                                                                                                                                                                    WPI; 2000-647075/62.
P-PSDB; AAB28406.
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                                                                                                                                                                                                                                Jefferson RA,
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The present sequence encodes a microbial beta-glucuronidase (GUS) protein. GUS genes were obtained from six different genera:
Enterobacter/Salmonella, Pseudomonas, Salmonella, Staphylococcus and Thermotoga. Microbial GUS can be used as a reporter/effector molecule for transgenic constructions and in in vitro diagnostic applications. It may also be used to generate sentinel plants that serve as bioindicators of

Claim 2; Fig 4; 116pp; English.

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Query Match
Best Local Similarity
Matches 1689; Conserv
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                                                                                                               Query Match
Best Local S
Matches 1688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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     Lagace RE, Spliv L
Xu Y, Kwong M, Po
        Mooney EM, Delegeane AM, Panesar IS, Banville SC, Red
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, C
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, St
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA,
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson
Patury S, Shi X, Suarez CJ;
                                                                                       Harthshorne TA,
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2002US-0410260P
                                                                                                   Wright RJ,
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                                                                       ght RJ, Bruns CM, Marjanovic MM, Shen F;
Suchorolski MT, Altus CM, Pitts SJ, Elder L
geane AM, Panesar IS, Banville SC, Reddy TP;
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                        Gietzen
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WPI; 2004-329368/30.
P-PSDB; ABM84772.
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New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.

Claim 1; Page; 190pp; English

disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp polymucleotide of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorder, developmental disorder, endocrine

Sequence 2050 BP; 465 A; 532 C; 598 G; 455 T; 0 U; 0 Other;

Length 2050;

Query Match Best Local

Similarity

Ş S Ś 밁 Ś B Ś 밁 Ş 5 밁 Ś В S 밁 밁 밁 밁 5 Matches 493; 1274 1295 1214 1235 1154 1175 1094 1115 1037 1055 977 995 917 935 875 815 797 737 GAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTACTACGGCTGGTACA TGGATCGAACACGCCCCGTTGTCATGGTGAGCATGATGGACGCACCAGACGAGAGAACAA AGTCCAACCATCCAGACGCGGAGGGTTTCTTCAAAGCCCCTTTATGAGACTGCCAATGAAA CAAGGTACCA---CTACAATCCCGAGACTCAGAAGATAGCAGAAGACAACATAAGAAGAA 1093 regarcinecceacaeacreegaarccinerearagaegaageeceegeaceinegratea 1036 TTCGCTGGCTTGGTGCCAACGCTTTCCGTACCAGCCACTACCCCTATGCAGAGGAAGTGA 1054 TGAAGTGGATCAACGCGAATTCTTTCAGGACCTCTCACTATCCTTACAGTGAAGAGTGGC TGGGGCCTGTGTCTGACTTCTACACACTCCCTGTGGGGATCCGCACTGTGGCTGTCACCA TGGAACTTGAAAAAGACGAGTACACTCTGGACATCGGAATCAGAACGATCAGCTGGGACG CGTCCCACCTAGAATCTGCTGGCTACTACTTGAAGATGGTGATCGCTCACACCAAATCCT CGCTGCCGCAGTTCTTCAACAACGTTTCTCTGCATCACCACATGCAGGTGATGGAAGAAG TGCAGATGTGTGACCGCTATGGGATTGTGGTCATCGATGAGTGTCCCGGCGTGGGCCTGG AATTCCCCGTTCTGGGGCAGGGCACCTTTATCCATTGATGATAAAAGACTTCAACCTTC AGAGCCAGTTCCTCATCAATGGGAAACCTTTCTATTTCCACGGTGTCAACAAGCATGAGG AGAAGAGGCTCTATCTGAACGGGAAACCTGTCTTTTTGAAGGGCTTTGGAAAGCACGACG Conservative 10.3%; Score 174; DB 13; Pred. No. 2.7e-43; 0; Mismatches 430; 21; Gaps 1333 1273 1114 1234 1174 874 994 934 856

1343

CAGACAAGGGGGCTCCGTATGTGGATGTGATCTGTTTGAACAGCTACTACTCTTGGTATC

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RESULT 4
ACN43423
ID ACN4
XX ACN4
XX ACN4
XX ACN4
XX B8;
KW G1th
XX G8;
KW G1th
XX Home
XX W S8;
KW G1th
XX Home
XX I2-5
PF 12-5
XX I2-5
PR 12-5
XX I2-5
PR 12-5
XX IX-6
PR 12-6
XX Schm
PI Hart
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Lagace RE, Sp. Xu Y, Kwong M, Po
The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human
                                                                                                                                                                              New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy oin gene mapping.
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Mooney EM, Del
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                                                                                                                                                                                                                                                                                                                                                                                                           , Wright RJ, Bruns CM, Marjanovic MM, Shen F; le TA, Suchorolski MT, Altus CM, Pitts SJ, Elder L. Delegeane AM, Panesar IS, Banville SC, Reddy TP; Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtcng M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Shi X, Suarez CJ;
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                                                                         TCCACTACGATCCACCTCAAATGTTCTCCGAAGAGTACCAAGCAGAGCTCGTTGAAAAG-
                                                                                                                   ATAAGAAGTATCAGAAGCCCATTATTCAGAGCGAGTATGGAGCAGAAACGATTGCAGGGT
                                                                                                                                                      ATGCAAGGCACAGAAAGCCCATCTTTGTCACAGAATTCGGTGCGGACGCGATAGCTGGCA 1453
                                                                                                                                                                                                                                 TCTATCAGGGAAGGATAGAAGAAGGACTTCAAGCTCTGGAAAAAAGACATAGAAGAGCTCT 1393
                                                                                                                                                                                                                                                                      CAGACAAGGGGGCTCCGTATGTGGATGTGATCTGTTTGAACAGCTACTACTTGGTATC 1434
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                                                                                                                                                                                             ACGACTACGGGCACCTGGAGTTGATTCAGCTGCAGCTGGCCACCCAGTTTGAGAACTGGT
                                                                                                                                                                                                                                                                                                                                                     TGGACCCCTCCCGGCCTGTGACCTTTGTGAGCAACTCTAACTATGCAG------
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Pred. No. 2.7e-43;
D; Mismatches 430;
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ACGATCAGGCTCCTTTTGAAAAA-----AGACTACATCATCGGAACACGCGTGTGGGCCT 156;

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Best Local Similarity
                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                     Sequence 2128 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic a
genes from Drosophila
interactions.
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11-JUL-2000; 2000US-00614150
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                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 6923; 21pp +
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ACAACGACAGCCTGCTGCTGAATGGAAAACCCCTCTATCTGCGGGGATTTGGACGGCACG
                             ACGAGAAGAGGCTCTATCTGAACGGGAAACCTGTCTTTTGAAGGGCTTTGGAAAGCACG
                                                                                                   AGGTGGAACTTGAAAAAGACGAGTACACTCTGGACATCGGAATCAGAACGATCAGCTGGG
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                                                                                                                                                  Score 174; DB 4;
Pred. No. 2.8e-43;
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02-APR-2003
                                                 AAD50922
                         mexicana SAP-human beta-GUS-IGF-II chimeric
                                                 standard;
                                (first
                                                 DNA;
                                entry)
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Lysosome; metabolic disease; lysosomal storage disease; gene therapy; Gaucher's disease; Pompe's disease; Hurler's syndrome; neuroprotective; Niemann-Pick's disease; Schindler's disease; mucollipidosis; cystinosis; Batten's disease; prosaposin; infantile neuronal ceroid lipofiscinosis; fucosidosis; mannosidosis; antilipaemic; insulin-like growth factor 2;

DNA.

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                                                                  Query Match
Best Local (
                             Matches
                                                                                 mucolipidosis, cystinosis, Batten's disease, prosaposin, or infantil neuronal ceroid lipofiscinosis. The invention is also useful in gene therapy. The present sequence is DNA encoding Leishmania mexicana secreted acid phosphatase (SAP) signal peptide, human mature beta-Gt (glucoronidase), linker and IGF-II chimeric protein. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                WPI;
                                                                 Sequence
                                                                                                                                        The invention relates to targetted therapeutic comprising a therapeutic agent that is active in a mammalian lysosome, and a means for binding an extracellular domain of human cation-independent mannose-6-phosphate receptor in a mannose-6-phosphate independent manner. The invention is useful for treating metabolic diseases such as lysosomal storage disease, e.g. Gaucher's disease, Pompe's disease, Hurler's syndrome, Niemann-pick's disease, mannosidosis, fucosidosis, Schindler's disease,
                                                                                                                                                                                                                   Example 1; Fig 3; 68pp; English
                                                                                                                                                                                                                                       receptor, useful storage disease.
                                                                                                                                                                                                                                              New targeted therapeutic that is active in a mammalian lysosome binds extracellular domain of human cation-independent mannose-6-phosphate receptor, useful for treating metabolic diseases such as lysosomal
                                                                                                                                                                                                                                                                                        P-PSDB;
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10-JUL-2001; 2001US-030460P.
15-OCT-2001; 2001US-0329461P.
23-JAN-2002; 2002US-0351276P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product= "Human
807. .1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "IGF-II sequence"
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TCACTCGGCAGAGACAACCAAAAAGTGCAGCGTTCCTTTTGCGA
                                              TCACAAGAGACAGACAACCCCAAACTCGTTGCTCATGTACTGAGA
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CC (GT) which comprised: (a) a therapeutic agent that is therapeutically active in human lysosome; and (b) a lysosomal targeting domain that binds an extracellular domain of human cation-independent mannose-6-phosphate creceptor (CM) and (i) does not bind a mutein in which amino acid 1572 of CM is changed from isoleucine to threonine; and (ii) binds the mutein CC with dissociation constant at least ten times the dissociation constant constant for binding CM. Also described: (1) an underglycosylated therapeutic constant constant in the binds to an extracellular domain and a subcellular compartment where of a cell, and upon internalisation of the receptor on an exterior surface of a cell, and upon internalisation of the receptor, compartment where the therapeutic domain to a subcellular compartment where the therapeutic domain is therapeutically active; and compartment where the therapeutic domain is therapeutically active; and constant of the patient. GT can be used for treating a lysosomal storage disease patient by administering FP con the patient. GT can be used for treating a patient by identifying a cative partient of the patient of the rapeutic agent that is considered that binds CM in a mannose-6-phosphate independent that is considered the patient, where the targeting moiety that binds of the patient, where the targeting moiety is identified by screening a nucleic acid or peptide library. GT is useful for treating constanting and constanting and constanting moiety is defects such as Pompe disease, Tay-Sachs disease, Sandhoff disease, Fabry disease, Gaucher disease, Batten disease, infantile neuronal ceroid
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sialic acid storage disease, Batten disease, infantile neuronal lipofuscinosis, Ehlers-Danlos syndrome type VI and congenital dof glycosylation. The present sequence is used in the exemplific
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05-JUN-2002; 2002US-0386019P.
06-SEP-2002; 2002US-0408816P.
16-OCT-2002; 2002US-00272531.
06-FEB-2003; 2003US-0445734P.
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                                                                                                                 ACCATCTGGGTCTGGATCAAAAACGCAGAAAATATGTGGTTGGAGAGCTCATTTGGAATT
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05-JUN-2002;
06-SEP-2002;
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10-JUL-2001;
15-OCT-2001;
23-JAN-2002;
The invention relates to a targetted therapeutic which comprises a therapeutic agent that is active in a mammalian lysosome and means for binding an extracellular domain of human cation-independent mannose-6 phosphate receptor in a mannose-6 phosphate-independent manner. The targetted therapeutic, therapeutic fusion protein and methods of the invention are useful for treating lysosome storage diseases. The invention is also useful in gene therapy. The present sequence is a fusion DNA used in the exemplification of the invention. This DNA encod a fusion protein which comprises a signal peptide sequence, a human mature beta-glucoronidase (GUS) sequence, a bridge of three amino acids
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2002US-0351276P.
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Pred. No. 2.
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Best Local
                                                                                                                                                   Matches 492;
                                                                                                                                                                                                                         The present invention relates to recombinant adeno-associated virus (AAV) expression vectors and virions, which include genes coding for enzymes defective or missing in lysosomal storage disease (LSD). AAV is useful in the manufacture of a medicament for treating lysosomal storage disease e.g., mucopolysaccharidoses VII (MPS VII). MPS VII (Sly Syndrome) is due to the deficiency in the lysosomal enzyme beta-glucuronidase (GUS) which aids in the breakdown of glycosaminoglycans (GAGs). AAV is used in gene therapy. The present sequence is human GUS DNA. This sequence is used in
                                                                                                                                                                                            Sequence 1956 BP; 437 A; 533 C; 563 G;
                                                                                                                                                                                                                                                                                                                          Disclosure; Page 77-80;
                                                                                                                                                                                                                                                                                                                                             Use of recombinant adeno-associated virus, comprising gene encoding a protein defective or missing in lysosomal storage disease, in the manufacture of a medicament for treating the lysosomal storage disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-1999;
30-JUN-2000;
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                                                                                   AGAAGAGGCTCTATCTGAACGGGAAACCTGTCTTTTTGAAGGGCTTTGGAAAGCACGAGG
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                                         AATTCCCCGTTCTGGGGCAGGGCACCTTTTATCCATTGATGATAAAAGACTTCAACCTTC
                                                             AGAGCCAGTTCCTCATCAATGGGAAACCTTTCTATTTCCACGGTGTCAACAAGCATGAGG
                                                                                                        TGGGGCCTGTGTCTGACTTCTACACACTCCCTGTGGGGATCCGCACTGTGGCTGTCACCA
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Pred. No. 8.4e-43;
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TCACTCGGCAGAGACAACCAAAAAGTGCAGCGTTCCTTTTGCGA
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                                                TCACAAGAGACAGACAACCCCAAACTCGTTGCTCATGTACTGAGA 1671
                                                                                                   TTGCCGATTTCATGACTGAACAGTCACCGACGAGAGTGCTGGGGAATAAAAAGGGGATCT
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RESULT 10
ABK83932
                              Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease;
granulocyte activation; chronic inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK83932 standard; cDNA; 2191
                                                                                                                                                                                                                                                                                                                                                                                                            14-AUG-2002
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                                                                                                                                                                                                                                                                                                                 CC DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where CC differential expression of Gs is indicative of GCA. Also included are CC expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a CC tissue, an allergic response in a subject, exposure of a subject to a CC pathogen or sterile inflammatory disease using the gene expression of the gene in a subject, exposure of a subject to a CC pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression in a subject, exposure of a subject to a gent that modulates the expression of gene(s) from Gs, where the level of inflammatory disease, by contacting a tissue having inflammation with an CC agent that modulates the expression of gene(s) from Gs, where the tissue of finflammation; (4) treating CC expression in a tissue; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an CC inflammation in a tissue; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an CC inflammation in a tissue; M3 is useful for detecting an inflammation of sepecially chronic) in a tissue, an allergic response in a subject to a pathogen or sterile inflammatory disease (e.g. capdiac reperfusion injury, renal reperfusion injury, as allows a schema, thrombosis, CC addiac reperfusion injury, renal reperfusion injury, as allows.

CC expressed in granulocytes. Note: The sequence after above this patent did cont form part of the printed specification, but was obtained in election of conditions. The present sequence represents a gene differentially control of the printed specification, but was obtained in election of conditions.
                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 492; Conser
                                                                                                                                                                                                                                                                       Sequence 2191 BP; 497 A; 589 C; 630 G; 475 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting granulocyte activation by detecting differential expression o genes associated with granulocyte activation, which serves as diagnosti markers that is useful for monitoring disease states and drug toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 503; 114pp; English
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                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
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 ATGCGGACATCCGAGGGAAGGGCTTCGACTGGCCGCTGCTGAAGGACTTCAACCTGC
                                                                                                 AGAAGAGGCTCTATCTGAACGGGAAACCTGTCTTTTTGAAGGGCTTTTGGAAAGCACGAGG
                                                                                                                                     TGGGGCCTGTGTCTGACTTCTACACACTCCCTGTGGGGATCCGCACTGTGGCTGTCACCA
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                              AATTCCCCGTTCTGGGGCAGGGCACCTTTTATCCATTGATGATAAAAGACTTCAACCTTC
                                                                 AGAGCCAGTTCCTCATCAATGGGAAACCTTTCTATTTCCACGGTGTCAACAAGCATGAGG
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                       10.2%;
                                                                                                                                                                                                                       Score 172.4; DB Pred. No. 9e-43;
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subject. the method comprises determining, in a sample from the subject, CC the level of at least one polypeptide, where a higher level of the CC polypeptide compared to the level of the polypeptide in a subject free of CC cancer is indicative of cancer. The polypeptide is selected from any of CC the polypeptides encoded by the polynucleotides listed in the CC specification and polypeptides which are at least 70% homologous to the CC polypeptides. The method of the invention has cytostatic activity, and CC may have a use in gene therapy. The method is useful in identifying CC markers specific for one or several types of cancer, depending on the CC interventions as well as cancer type-specific targets for therapeutic CC applications as well as cancer type-specific targets for therapeutic CC intervention. The compounds that modulate the activity of a tumour CC drugs. The present sequence represents a polynucleotide of the invention XX
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The invention relates to a method of predicting clinical outcome is patient diagnosed with cancer by determining the expression level or more genes, or their expression products, selected from p53BP2, cathepsin B, cathepsin L, Ki67/MiB1, and thymidine kinase in a car tissue obtained from the patient, normalized against control generates the patient of the patient

reference

cancer tissue set.

gene(s), cancer

and

of. one

tissue obtained compared to the

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ADG89395
ID ADG893
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                                                                                                                                                                                                                                                               Predicting clinical outcome for a patient determining the expression level of one out the amount found in a reference cancer tis
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18-SEP-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       r; gene expression; receptor-positive i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; DNA;
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ACGATCAGGCTCCTTTTGAAAAA-----AGACTACATCATCGGAACACACGTGTGGGCCT
                                                                   TTCACCAGGATCCACCTCTGATGTTCACTGAAGAGTACCAGAAAAGTCTGCTAGAGCAGT
                                                                                                                 TCCACTACGATCCACCTCAAATGTTCTCCGAAGGAGTACCAAGCAGAGCTCGTTGAAAAG-
                                                                                                                                                                                                               ATAAGAAGTATCAGAAGCCCATTATTCAGAGCGAGTATGGAGCAGAAACGATTGCAGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                          TCTATCAGGGAAGGATAGAAGAAGACTTCAAGCTCTGGAAAAAGACATAGAAGAGCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGAAGTGGATCAACGCGAATTCTTTCAGGACCTCTCACTATCCTTACAGTGAAGAGTGGC
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52.1%;
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Pred. No. 9e
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                                                  The present invention relates to a polypeptide comprising an antiangiogenesis polypeptide region linked to a therapeutic protein or CC polypeptide region, or a diagnostic protein or polypeptide region. The CC polypeptide comprising an antiangiogenesis polypeptide region or the CC nucleic acid encoding the polypeptide comprising the antiangiogenesis of polypeptide is useful for diagnosing or treating angiogenesis-dependent CC diseases or cancer. Angiogenesis-dependent diseases include age-related CC macular degeneration, artherosclerosis, angiofibroma, neovascular CC glaucoma, arteriovanous malformations, nonunion fractures, arthritis, CC rheumatoid arthritis, lupus, connective tissue disorders, Osler-Weber CC syndrome, psoriasis, corneal graft neovascularisation, pyogenic CC granuloma, delayed wound healing, retrolental fibroplasia, diabetic CC granuloma, televoderma, granulations, haemangioma, trachoma, cCC haemophilic joints, vascular adhesions, hypertrophic scars, multiple sclerosis, restenosis or obesity. The present sequence is a coding ccc sequence shown in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide comprising an antiangiogenesis polypeptide region linked to a therapeutic protein or a diagnostic protein, useful for diagnosing or treating angiogenesis-dependent diseases e.g. cancer, lupus or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein targeting; angiogenesis inhibitor; fusion gene; cancer; gene; antiangiogenic; cytostatic; ophthalmological; antiarthritic; antiinflammatory; dermatological; immunosuppressive;
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Novel viral vector comprising beta-catenin/bipartite T-cell factor-responsive promoter having first and second promoter region linked target nucleic acid sequence, useful for treat- ing colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; beta-catenin activity inhibitor; gene therapy; colon metastasis; liver; thymidine kinase; prodrug; chemotherapy; radiation therapy; surgery; human; beta-glucuronidase; gene; ds.
                                                                                          WPI; 2004-042209/04
                                                                                                                                                                                                (HUNG/)
                                                                                                                                                                                                                                                                03-MAY-2002; 2002US-0377672P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human beta-glucuronidase
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KWONG K

ZOU Y.
                                                                                                                                 Kwong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bipartite T-cell factor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tcf; promoter construct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treatment
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This invention relates to a novel viral vector comprising a betaCC catenin/bipartite T-cell factor (Tcf) responsive promoter construct which
CC contains a first promoter region having a copy of Tcf/LEF-1 binding site
CC contains a first promoter region having a copy of Tcf/LEF-1 binding site
CC contains a first promoter region and a nucleic acid
CC sequence, where the first and second promoter regions are operatively
CC linked to target nucleic acid sequence. The invention may be useful for
CC the development of compounds with a cytostatic activity, through action
CC may be useful for treating an individual with colon cancer which is
CC metastasised to the liver. The treatment involves administering the
CC vector of the invention where the nucleic acid sequence encodes a
CC therapeutic polypeptide or thymidine kinase, a prodrug and chemotherapy,
CC radiation, surgery or gene therapy to the individual. The present
CC sequence is that of a therapeutic gene which may be used in the vector of
CC the invention for the treatment of an individual with cancer.

Sequence 2191 BP; 497 A; 589 C; 630 G; 475 T; 0 U; 0 Other;

Similarity

10.2%;

DB 12;

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TGCAGATGTGTGACCGCTATGGGATTGTGGTCATCGATGAGTGTCCCGGCGTGGGCCTGG
                                                                                                                             TGAAGTGGATCAACGCGAATTCTTTCAGGACCTCTCACTATCCTTACAGTGAAGAGTGGC
                                                                                                                                                                                         ATGCGGACATCCGAGGGAAGGGCTTCGACTGGCCGCTGCTGAAGGACTTCAACCTGC
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                                                                                                                                                                                                                                                                                                                                                                               TGGGGCCTGTGTCTGACTTCTACACACTCCCTGTGGGGATCCGCACTGTGGCTGTCACCA
                                            TGGATCTTGCCGACAGACTCGGAATCCTTGTGATAGACGAAGCCCCGCACGTTGGTATCA 1036
                                                                                                                                                                                                                                     AATTCCCCGTTCTGGGGCAGGGCACCTTTTATCCATTGATGATAAAAGACTTCAACCTTC
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   Wohlgemuth J, Rosenberg S;
                                                                                                                                                  24-APR-2002; 2002US-00131831.
20-DEC-2002; 2002US-00325899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transplant rejection; immune system; rheumatoid arthritis; inflammatory bowel disease; multiple sclerosis; HIV; AIDS;
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Diagnosing or monitoring transplant rejection, e.g. heart, kidney, live pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level
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Claim 80; SEQ ID NO 335; 1762pp; English

The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lung, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a many areference sequence for a 50 mer oligonucleotide marker for diagnosis and monitoring of allograft rejection and other disorders.

Sequence 2191 BP; 497 A; 589 C; 630 G; 475 T; 0 U; 0 Other;

Matches 492; Query Match

Conservative

<u>.</u>

431;

Indels Length

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Gaps

Local Similarity

10.2%;

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                                                         CAGACAAGGGGGCTCCGTATGTGGATGTGATCTGTTTGAACAGCTACTACTCTTGGTATC
                                                                                          GAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTACTACGGCTGGTACA 1333
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Search completed: September 1, 2005, 22:25:44 Job time : 985 secs

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Result
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CN155220 942501 MA
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ALIGNMENTS

y Match Local Similarity 52.2%; Pred. No. 7.7e-40; hes 493; Conservative 0; Mismatches 430	Query Match Best Local
/organism="Homo sapien /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSODL001YM21" /tissue_type="B_cells /plasmid="pCMVSPORT_6"	ORIGIN
Location/Qualifiers	FEATURES source
web: www.genoscope.cns.rr) 1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a distinct of Technologies, a	COMMENT
2 (bases 1 to 1377) Genoscope. Direct Submission Submitted (20-JUL-2004) G BP 191 91006 EVRY cedex -	REFERENCE AUTHORS TITLE JOURNAL
Full-length cDNA libraries and normalization Unpublished Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue	_
Homo sapiens Bukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1377) Li,W.B., Gruber,C., Jessee,J.	RCE 5
CR593823.1 GI:50474630 CR593823.1 GI:50474630 HTC; CNSLT_cDNA. Homo sapiens (human)	
CR593823 1377 bp mRNA full-length cDNA clone CSODL001YM21 of B cCCt 25-normalized of Homo sapiens (human).	z
SO POLITE II SAMEBIA OLI EE BAG OCL	CR593823 1377 bp mRNA linear HTC 21-JUL-200 full-length cDNA clone CSODL001YM21 of B cells (Ramos cell line) Cot 25-normalized of Homo sapiens (human). CR593823.1 GI:50474630 HTC; CNSLT_cDNA. HOMO sapiens (human) HOMO sapiens (buman) HOMO sapiens (buman) HOMO sapiens (buman) 1 (base I to 1377) 1 (bases I to 1377) 1 (bases I to 1377) Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue 2 (bases I to 1377) Genoscope. Direct Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr Waw.genoscope.cns.fr 1 st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and clones that strand cDNA was constructed by Life Technologies, a division of Invitrogen. Location/Qualifiers 1 .1377 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="CSODL001YM21" /tissue_type="B cells (Ramos cell line) Cot 25-normalized / plasmid="pCMVSPORT_6" 10.3%; Score 174; DB 3; Length 1377;

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215 TGGGGCCTGTGTCTGACTTCTACACACTCCCTGTGGGGATCCGCACTGTGGCTGTCACCA 274

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RESULT 2
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90135266 Single gene library
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Primates;
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 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Genomics 83 (4), 566-571
Contact: Jin, P.
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Fax: 650 621 8965
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                                                                                   GAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTACTACGGCTGGTACA
   ACGACTACGGGCACCTGGAGTTGATTCAGCTGCAGCTGGCCACCCAGTTTGAGAACTGGT
                               TCTATCAGGGAAGGATAGAAGAAGGACTTCAAGCTCTGGAAAAAAGACATAGAAGAGCTCT
                                                                 CAGACAAGGGGGCTCCGTATGTGGATGTGATCTGTTTGAACAGCTACTACTCTTGGTATC
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Pred. No. 8.5e-40;
D; Mismatches 430;
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1 (bases 1 to 1853)
Jin,P., Fu,G.K., Wilson,A.D., Yang,
Au-Young,J. and Stuve,L.L.
PCR isolation and cloning of novel
/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone lib="Single gene library"
/clone lib="Single gene library"
/note="Vector: pDrive Cloning Vector; RT-PCR was performed using gene-specific primers flanking the open-reading frame. PCR products were subcloned into pDrive Cloning Vector and sequenced completely using M13 forward and reverse primers. Sequencing gaps were closed by re-sequencig using primers flanking the gapped areas."
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TGGAACTTGAAAAAGACGAGTACACTCTGGACATCGGAATCAGAACGATCAGCTGGGACG Length 1853; Indels 21; Gaps

TTCGCTGGCTTGGTGCCAACGCTTTCCGTACCAGCCACTACCCCTATGCAGAGGAAGTGA TGAAGTGGATCAACGCGAATTCTTTCAGGACCTCTCACTATCCTTACAGTGAAGAGTGGC ATGCGGACATCCGAGGGAAGGGCTTCGACTGGCCGCTGCTGGTGAAGGACTTCAACCTGC AATTCCCCGTTCTGGGGCAGGGCACCTTTTATCCATTGATGATAAAAGACTTCAACCTTC AGAAGAGGCTCTATCTGAACGGGAAACCTGTCTTTTTGAAGGGCTTTGGAAAGCACGAGG TGGGGCCTGTGTCTGACTTCTACACACTCCCTGTGGGGATCCGCACTGTGGCTGTCACCA AGAGCCAGTTCCTCATCAATGGGAAACCTTTCTATTTCCACGGTGTCAACAAGCATGAGG 683 863 803 743

CAAGGTACCA---CTACAATCCCGAGACTCAGAAGATAGCAGAAGACAACATAAGAAGAA CGTCCCACCTAGAATCTGCTGGCTACTACTTGAAGATGGTGATCGCTCACACCAAATCCT AGTCCAACCATCCAGACGCGGAGGGTTTCTTCAAAGCCCTTTATGAGACTGCCAATGAAA TGGACCCCTCCCGGCCTGTGACCTTTGTGAGCAACTCTAACTATGCAG------TGGATCGAACACGCCCCGTTGTCATGGTGAGCATGATGGACGCACCAGACGAGAGAACAA TGGTGCGTAGGGACAAGAACCACCCCGCGGTCGTGATGTGGTCTGTGGCCAACGAGCCTG CGCTGCCGCAGTTCTTCAACAACGTTTCTCTGCATCACCACATGCAGGTGATGGAAGAAG 1273 1213 1153 1093 1043 983

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Best Local Similarity
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Genomics 83 (4), 566-571
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1 (bases 1 to 1995)

Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R., Au-Young,J. and Stuve,L.L.

PCR isolation and cloning of novel splice variant mRNAs from k
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90134967 Single gene li
CD014092
CD014092.1 GI:37777621
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Jin, P
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AATTCCCCGTTCTGGGGCAGGGCACCTTTTATCCATGATGATAAAAGACTTCAACCTTC
                                       AGAGCCAGTTCCTCATCAATGGGAAACCTTTCTATTTCCACGGTGTCAACAAGCATGAGG
                                                              AGAAGAGGCTCTATCTGAACGGGAAACCTGTCTTTTTGAAGGGCTTTGGAAAGCACGAGG
                                                                                         TGGGGCCTGTGTCTGACTTCTACACACTCCCTGTGGGGATCCGCACTGTGGCTGTCACCA
                                                                                                                    TGGAACTTGAAAAAGACGAGTACACTCTGGACATCGGAATCAGAACGATCAGCTGGGACG
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650 621 8965
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Location/Qualifiers
                                                                                                                                                                                                       /clone lib="Single gene library"
/notes "Vector: pDrive Cloning Vector; RT-PCR was performed using gene-specific primers flanking the open-reading frame. PCR products were subcloned into pDrive Cloning Vector and sequenced completely using M13 forward and reverse primers. Sequencing gaps were closed by re-sequencing using primers flanking the gapped areas."
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/db_xref="taxon:9606"
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Pred. No. 8.8e-40;
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CD503076 1124 bp mRNA linear EST 12-CDA60-CO7.x1d-t SHGC-CDA Gasterosteus aculeatus cDNA clone CDA60-CO7 5', mRNA sequence.
CD503076 Kingsley,D.M., Peichel,C., Balabahdra,S., Schmutz,J. and Myers,R.M.
Expressed sequence tags from Gasterosteus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes; Gasterosteidae; Gasterosteidae; Gasterosteidae; Gasterosteus.

1 (bases 1 to 1124) Gasterosteus aculeatus CD503076.1 EST. Gasterosteus aculeatus (three spined stickleback) GI:31432977 Grimwood, J., EST 12-JUN-2003 Dickson, M.

Gasterosteus

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Kingsley, DM
HHMI and Department of Developmental Biology
Stanford University School of Medicine
Beckman Center B300, 279 Campus Drive, Stanfor
Tel: 650 725 5954
Pax: 650 725 739
Email: kingsley@cmgm.stanford.edu
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CCTCCTGCTGATTACTATTTCAAAACCTTGATAAAACATACCAAAGAATTGGATCCAACC
                                     CCAGACGCGGAGGGTTTCTTCAAAGCCCTTTATGAGACTGCCAATGAAATGGATCGAACA 122
                                                                                 GACAAGAACCATCCCTCTGTGGTCATGTGGTCAGTGGCCAATGAGCCGGCTGCAGAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: lambda ZAP Express/pBK-CMV; Site 1: EcoR1 (5' adaptor); Site 2: KhoI (3' linker primer); The mixed organ cDNA library was generated using the ZAP-CDNA method by Stratagene. First strand cDNA synthesis was primed with a a 50 bp linker primer containing an oligo dT sequence preceded by a synthetic XhoI site. 5 prime adaptors were used containing an EcoRi cohesive end. The finished cDNAs were inserted in to the ZAP express vector unidirectionally in the sense orientation with respect to the lacZ promoter of pBK-CMV. An amplified library was prepared from approximately 3 million primary clones in the lambda ZAP Express vector. In vivo excision was then the lambda ZAP Express vector. In vivo excision was then
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used to generate individual pBK-CMV phagemid clones for {\tt EST} sequencing."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="Salinas river,
/db_xref="taxon:69293"
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/tissue_type="heads and internal organs
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                                                                                                                                                                                                                                                                                                                                                                                                                                 HHMI and Department of Developmental Biology Stanford University School of Medicine Beckman Center B300, 279 Campus Drive, Stanf Tel: 650 725 5954 Fax: 650 725 7739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteidae; Gasterosteidae; Gasterosteus.

1 (bases 1 to 1138)
1 (bases 1 to 1138)
2 (chance) D.M., Peichel C., Balabahdra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.

Expressed sequence tags from Gasterosteus aculeatus
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDA60-D07.x1d-t SHGC-CDA Gasterosteus CDA60-D07 5', mRNA sequence.
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CD503098.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCACCTCAAATGTTCTCCGAAGAGTACCA-----AGCAGAGCTCGTTGAAAAGACGATC 1518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGAAACCCATCATCCAGAGCGAATACGGAGCGGATGCGGTGCCGGGGCTTCACAGTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGATAGAAGAAGGACTTCAAGCTCTGGAAAAAGACATAGAAGAGCTCTATGCAAGGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGACTCCTCAGAATGTGAGAAGACCCATTCTCAACCACAAGGGTGTTTTCACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCACCCGTGATGTTTACTGAGGAGTACCAGAAGTTAGTCCTGCAGAGCTACCACAACGTG
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                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: 782
                                                                                                                                                                                                                                                                                                                                                                                                            kingsley@cmgm.stanford.edu
/clone lib="SHGC-CDA"
/clone lib="SHGC-CDA"
/note="Vector: lambda ZAP Express/pBK-CMV; Site 1: EcoRl
/note="Vector: lambda ZAP Express/pBK-CMV; Site 1: EcoRl
(5' adaptor); Site 2: XhoI (3' linker primer); The mixed
organ cDNA library was generated using the ZAP-cDNA method
by Stratagene. First strand cDNA synthesis was primed with
a a 50 bp linker primer containing an oligo dT sequence
                                                                                                                                     tissue_type="heads and internal organs/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="Salinas river,
/db_xref="taxon:69293"
                                                                                                                                                                                          /sex="mixed male and female"
                                                                                                                                                                                                                                                                                                organism="Gasterosteus aculeatus"
                                                                                                                                                                                                               clone="CDA60-D07"
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AGACTCCTCAGAATGTGAGAAGACCCATTCTCAACCACAAGGGTGTTTTCACAAGAGACA
                                                                                                                                                                                                                                                              CCACCTCAAATGTTCTCCGAAGAGTACCAAGCAGAGCTCGTTGAAAAAGACGATCAGGCTC
                                                                                                                                                                                                                                                                                                                                                             AGAAAGCCCATCTTTGTCACAGAATTCGGTGCGGACGCGATAGCTGGCATCCACTACGAT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGAAGTACTTCGACATCGTCTGTGTAACAGGTACTACGGCTGGTACATCTATCAGGGA 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGACGCGGAGGGTTTCTTCAAAGCCCTTTATGAGACTGCCAATGAAATGGATCGAACA 1224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAGACGAGTACACTCTGGACATCGGAATCAGAACGATCAGCTGGGACGAGAAGAGGCTC
                                                                                                                                                                                                         CCACCCGTGATGTTTACTGAGGAGTACCAGAAGTTAGTCCTGCAGAGCTACCACAACGTG
                                                                                                                                                                                                                                                                                                                      CAGAAACCCCATCATCCAGAGCGAATACGGAGCGGATGCGGTGCCGGGGCTTCACAGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                   CACCCGGAGGTCATCCCATCCAGCTCAACACTCAGTTTGAGAACTGGTACGGAAAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGATAGAAGAAGGACTTCAAGCTCTGGAAAAAGACATAGAAGAGCTCTATGCAAGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTCCCTACGTGGACGTCATCTGCGTAAACAGTTACTTCTCCTGGTACCATGACCCGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTCCTGCTGATTACTATTTCAAAACCTTGATAAAACATACCAAAGAATTGGATCCAACC 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTTTTGGAAACGCCTCCTTAACCCATCACCTGGTCGTCATGGACGAGCTGGTACGTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACTACAATCCCGAGACTCAGAAGATAGCAGAAGAACATAAGAAGAATGATCGACAGA 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACCGCCATGGCATCGTGATAGACGAGTGCCCGGGCGTGGGCATAAAAGACATTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACAGACTCGGAATCCTTGTGATAGACGAAGCCCCGCACGTTGGTATCACA---AGGTAC 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGGCCAACTCGTTCCGCACCAGCCACTACCCTTATGCAGAGGAGATCCTGCAGATGTGT
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                                                                                                                                                   CTTTTGAAAAAAG----ACTACATCATCGGAACACGTGTGGGCCTTTGCAGATTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGAGGCAAAGGCCTGGACTGGCCCCTCATGGTGAAGGACTTTAACTTATTGAAGTGGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preceeded by a synthetic XhoI site. 5 prime adaptors were used containing an EcoR1 cohesive end. The finished cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              i to generate individual pBK-CMV phagemid clones for
sequencing."
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Pred. No. 4.7e-36;
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                       S Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramotto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakai, K., Sakazume, N., Okazaki, Y., Sasto, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                             Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2274)
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  Submitted (16-JUL-2001) Yoshihide Hayashizaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSN RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokokanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, WIL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222,
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3B|NM_010368, evidence: BLASTN, 99%,
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L.
Nonneman, D.J., Wray, J.E. and Keele, J.W.
Porcine EST collection using a normalized library
embryos representing early developmental stages
Unpublished (2003)
                                                                                                                                                                                                                                                                                           Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called
trimmed with the aid of the trim_alt
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Plate: TMW8042 row: M column: 18
Seq primer: GTAATACGACTCACTATAGGG.
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Mammalia; Eutheria;
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PO Box 166, Clay Center, N
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/clone_lib="MARC 4FIG"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
/ibrary made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
                                                                                                                                                                                                                 Location/Qualifiers
                                                                                          tissue_type="pooled"
'lab_host="DH10B"
                                                                                                                                      'mol_type="mRNA"
'db_xref="taxon:9823"
                                                                                                                                                       organism="Sus scrofa"
/mol_type="mRNA"
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                                                                         lib="MARC 4PIG"
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AGENCOURT 8741562 NIH_MGC_18
5', mRNA sequence.
80941196
BQ941196.1 GI:22356674
1 (bases 1 to 906) NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
Unpublished (1999)
                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                     Homo sapiens
                                                                                                                   Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://image.llnl.gov
Plate: LLCM2594 row: g column: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTTTGAAGGGCTTTGGAAAGCACGAGGAATTCCCCCGTTCTGGGGCAGGGCACCTTTTA 887
   GCAGCTGGCCACCCAGTTTGAGAACTGGTATAAGAAGTATCAGAAGCCCATTATTCAGAG
                                AGCTCTGGAAAAAGACATAGAAGAGCTCTATGCAAGGCACAGAAAGCCCATCTTTGTCAC 142
                                                                                    CTGTGTGAACAGGTACTACGGCTGGTACATCTATCAGGGAAGGATAGAAGAAGGACTTCA 1364
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                                                                 CTGTTTGAACAGCTACTACTCTTGGTATCACGACTACGGGCACCTGGAGTTGATTCAGCT
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6420519"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
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Pred. No. 4.5e-31;
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TGGGTGCCAACGCCTTCCGCACCAGCCACTACCCCTACGCAGAGGAGGTGATGCAGCTCT

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JOURNAL COMMENT
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ORGANISM
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CN155220
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Matches 425;
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                                                                                                                                                                       Query Match
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Sus scrofa
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942501 MARC 4PIG Sus scrofa c
CN155220 CN155220.1 GI:46169650
EST.
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Plate: TMW8046 row: I column: 19
Seq primer: GTAATACGACTCACTATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single pass sequencing. Bases called with trimmed with the aid of the trim_alt optic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: smith@email.marc.usda.gov
Single pass sequencing. Bases ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, US
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2003)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Nonneman, D.J., Wray, J.E. and Keele, J.W. Nonneman, D.J., Wray, J.E. and Keele, J.W. Porcine EST collection using a normalized library coembryos representing early developmental stages embryos representing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
   TCAACGCGAATTCTTTCAGGACCTCTCACTATCCTTACAGTGAAGAGTGGCTGGATCTTG
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                                                                                 TTCTGGGGCAGGCACCTTTTATCCATTGATGATAAAAGACTTCAACCTTCTGAAGTGGA
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                                                            TCCGAGGCAAGGGCTTTGACTGGTCGCTGCTGGTGAAGGACTTCAACCTGCTCCGCTGGC
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                                                                                                                                     Conservative
                                                                                                                                                                                                                            Library
day-15,
                                                                                                                                                                                                                          /clome_lib="MARC 4PIG"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: Not
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: Not
/lay-13; day-10; day-13; Site_1: BcoRI; Site_2: Not
/day-15; day-25; and day-30 whole embryos."
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                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9823"
/tissue_type="pooled"
                                                                                                                                                                                                                                                                                                                                                                         organism="Sus scrofa"
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                                                                                                                                                    8.4%;
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                                                                                                                               Score 142.6; D
Pred. No. 1.5e-
0; Mismatches
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No. 1.5e-30;
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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1051)

S Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization

L Unpublished (2001)

LOn May 5, 2003 this sequence version replaced gi:30372720.

Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Crue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
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BX363460 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CSODL001YM21 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                 BX363460.2
                                                                                                                                                                                                                                             Homo sapiens (human)
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For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODL001AG11QP1&c=4169.r.
                                                                                                                                                                                                                                       TGGATCGAACACGCCCCGTTGTCATGGTGAGCATGATGGACGCACCAGACGAGAGAACAA 1273
ATGCAAGGCACAGAAAAGCCCCATCTTTTGTCACAGAATTTCGGTGCGGACGCGATA-GCTGGC 1452
                                                                                                                                    CAGACAAGGGGGCTCCGTATGTGGATGTGATCTGTTTGAACAGCTACTACTCTTGGTATC
                                                                                                                                                                       GAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTACTACGGCTGGTACA 1333
                                                                                                                                                                                                                                                                                                                         AGTCCAACCATCCAGACGCGGAGGGTTTCTTCAAAGCCCCTTTATGAGACTGCCAATGAAA
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                                                           ACGACTACGGGCACCTGGAGTTGATTCAGCTGCAGCTGGCCACCCAGTTTGAGAACTGGT
                                                                                              TCTATCAGGGAAGGATAGAAGAAGGACTTCAAGCTCTGGAAAAAGACATAGAAGAGCTCT
                                                                                                                                                                                                                                                                                        CGTCCCACCTAGAATCTGCTGGCTACTACTTGAAGATGGTGATCGCTCACACCAAATCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATTCCCCGTTCTGGGGCAGGGCACCTTTTATCCATTGATGATAAAAGACTTCAACCTTC
                                                                                                                                                                                                             TGGACCCCTCCCGGCCTGTGACCTTTGTGAGCAACTCTAACTATGCAG--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR veites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) 25-NORMALIZED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="CSODL001YM21"
/cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED'
/cell_line="RAMOS CELL LINE"
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/mol_type="mRNA"
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50.7%;
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Pred. No. 3.2e-30
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 767)
Wittzell,H., Bed-Hom,B., Morin,V., Young,J.R., Whittaker,C.J., Chausse,A.M. and Zoorob,R.
A collection of chicken ESTs from activated immune cells Unpublished (2003)
Contact: Zoorob R
UPR 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mdvn127 c10_r2 Marek
cDNA, mRNA sequence.
CF255373
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Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 33 1 49 58 35 00 Fax: 33 1 49 58 33 81 Email: zoorob@vjf.cnrs.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CF255373.1 GI:33488628
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                                                                                                                                                                                                          GCGAATTCTTTCAGGACCTCTCACTATCCTTACAGTGAAGAGTGGCTGGATCTTGCCGAC
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                                          GCAAACTCCTTCCGTACCAGCCACTACCCCTATGCTGAGGAGATCATGGACCTGTGTGAC
                                                                                                                                                                                                                                                                     GGCAAAGGCCTGGACTGGGCACTGATCGTTAAGGACTTCAACCTGCTGCGCTGGTTGGGG
                                                                                                                                                                                                                                                                                                                GGGCAGGGCACCTTTTATCCATTGATGATAAAAGACTTCAACCTTCTGAAGTGGATCAAC
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TTTGGGAACAAATCTCTACAGCATCATCTCGTCGTGATGGAGGAACTGATCCGCAGGGAT
                                                                                         ACCTACGGCATTGTGGTGATCGACGAGTGCCCGGGCGTGGGGATTAAGATGCCTGAGAGC
                                                                                                                        AGACTCGGAATCCTTGTGATAGACGAAGCCCCGCACGTTGGTATCACAAGG---TACCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Gallus gallus"
/mol type="mRMA"
/db_xref="reaxon:9031"
/clone_lib="Marek's disease virus-infected
/note="Organ: Spleen; Vector: pTriplEX2"
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Pred. No. 1.4e-27;
0; Mismatches 364;
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CA453907
CA453907.1 GI
                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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AGENCOURT_10738557 MAPCL
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National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                    High
                                                                                                                                                                                                                                                                                                                                                      Plate: LLAM14275 row: a column: 17
                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 846)
                                                                                                                                                                                                                                                                                                                                quality sequence stop: 708.
            /clone lib="MAPCL"
/note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I;
/note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
cancer genes encoding
                                                                                                                                                                            hTERT-HME1,
                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                         organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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                                                                                                                                                                                          lone="IMAGE:6718553"
ell_line="ZR-75-1, MCF7,
                                                                                                                                                       host="EMDH10B"
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CA489317.1
EST.
Homo sapiens
                                                        mRNA sequence.
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nilarity 52.4%;
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sapiens (human)
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Pred. No. 4.4e-27;
D; Mismatches 356
                                                                                               Homo
                                                                                                                 900 bp
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM14283 row: d column: 20
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 900)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop:
                         CGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTACTACGGCTGGTACATCTATCAGG
                                                                                                                              CACGCCCCGTTGTCATGGTGAGCATGATGGACGACCACCAGACGAGAGAACAAGAGACGTGG 128:
                                                                                                                                                                          TAGAATCTGCTGGCTACTACTTGAAGATGGTGATCGCTCACACCAAATCCTTGGACCCCT
                                                                                                                                                                                                                    ATCCAGACGCGAGGGTTTCTTCAAAGCCCTTTATGAGACTGCCAATGAAATGGATCGAA 1222
                                                                                                                                                                                                                                                                                                    AGTTCTTCAACAACGTTTCTCTGCATCACCACATGCAGGTGATGGAAGAAGTGGTGCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGACCGCTATGGGATTGTGGTCATCGATGAGTGTCCCGGCGTGGGGCCTGGCGCTGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCGACAGACTCGGAATCCTTGTGATAGACGAAGCCCCGCACGTTGGTATCACAAGGTACC 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAACGCGAATTCTTTCAGGACCTCTCACTATCCTTACAGTGAAGAGTGGCTGGATCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCTGGGGCAGGGCACCTTTTATCCATTGATGATAAAAGACTTCAACCTTCTGAAGTGGA 925
GGGCTCCGTATGTGGATGTGATCTGTTTGAACAGCTACTACTCTTGGTATCACGACTACG
                                                                                     CCCGGCCTGTGACCTTTGTGAGCAACTCTAACTATGCAG---
                                                                                                                                                                                                                                                                GGGACAAGAACCACCCCGCGGTCGTGATGTGGTCTGTGGCCAACGAGCCTGCGTCCCACC
                                                                                                                                                                                                                                                                                                                                                                                              A---CTACAATCCCGAGACTCAGAAGATAGCAGAAGACATAAGAAGAATGATCGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGGTGCCAACGCTTTCCGTACCAGCCACTACCCCTATGCAGAGGAAGTGATGCAGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: DCMV-SPORT6; Site_1: ECORV; Site_2: Not I; Subtracted with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Egland, James J. Vincent, Robert Strausberg, Bungkook Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_line="ZR-75-1, MCF7, hTERT-HME1, LNCap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6721700"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
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Pred. No. 1e-26;
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CB203472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CB203472 914 bp mRNA 1
AGENCOURT 11297304 NIH MGC 135 Mus musculus
IMAGE:30141354 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1. (bases 1 to 914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: NDAM0048 row: n column: 19 High quality sequence stop: 580.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCTGGATCAAAAACGCAGAAAATACGTGGTTGGAGAGCTCATTTGGAAATTTGCCGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCCTTTTGAAAAAAG-----ACTACATCATCGGAACACACGTGTGGGGCCTTTGCAGATT 1576
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                                                                  /mol type="mRNA"

/db xref="taxon:10090"
/clone="IMAGE:30141354"

/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/clone=lib="NIH_MGC 135"
/clone="Weetor: pCMWSport6.1; Site 1: EcoRV; Site 2: Not1;
/nore="Veetor: pCMWSport6.1; Site 1: EcoRV; Site 2: Not1;
/norealized full-length enriched library from pooled mouse embryonic limb, maxilla and mandible, day 12.5, 13.5,
14.5, and 15.5 (size selected for the 0.5-1 kb fragments)
Cloned directionally, priming method: Oligo-dr. cDNA enrichment: >1k bp, Average insert size 1.6k bp.
Normalization (Cot value): 7.5 kb. Priming sequence:
5'GACTAGTTCTAGATCGCGAGCGGCCCC(T)3' Tissue contributed
                   by, David
Corp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus'
                                                 Rowe. Library constructed by ResGen, Invitrogen
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Query Match Best Local Similarity

7.7%;

Matches 410;

Conservative

0

Score 129.8; DB Pred. No. 1e-26; 0; Mismatches 3

DB 6; 382;

Length

914; 21;

Gaps

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REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                     RESULT 15
CO394571
LOCUS
                                                                                                                                                                                                             ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                  DEFINITION
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1 (bases 1 to 862)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                     CO394571
CO394571.1 GI:49576487
EST.
                                                                                                                                                                                                                                                   CO394571 862 bp mRI
AGENCOURT 27822917 NIH MGC 252 Rattus
IMAGE: 307606 5', mRNA sequence.
                                                                                                                                                                Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                        CAGCCCAAAACTTCGGCCTTTATTTTGCGAAGA 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATCAGAAACGTAAAGAATACGTGGTCGGAGAGCTCATCTGGAATTTCGCCGACTTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCCTTTTGAAAAAAGACTACATCATCGGAACACACGTGTGGGCCTTTGCAGATTTTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCGCCGCATATTACTTTAAGACGCTGATCACCCACACCAAAGCCCTGGACCTCACCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCAAATTCCTTTCGTACCAGCCACTATCCCTACTCAGAGGAGGTACTTCAGCTCTGTGAC
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTGAAGTGGATCAACGCGAATTCTTTCAGGACCTCTCACTATCCTTACAGTGAAGAGTG
                                                                                                                                                                                                                                                      GCTGGATCTTGCCGACAGACTCGGAATCCTTGTGATAGACGAAGCCCCGCACGTTGGTAT 1034
                            CCTGGACCCCACCCGTCCTGTGACCTTTGTGAGCAATA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="NIH MGC 252"
//clone lib="NIH MGC 252"
//note="Organ: ovary; Vector: pDONR 201; Site 1: Not1;
Site 2: Not1; RNA obtained from female overies animals at 8 km cold. Tissues were snap-frozen and kept at -80C for two days before RNA extraction and purification (Tri-reagent method). cDNA was primed using oligo-dT primer: 5'-pgACTAGTTCTAGATCGCGAGCGGCCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1.
Size-selection >1.25kb resulted in an average insert size of 1.7kb. This primary library is not normalized (normalized library is NIH MGC 252) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC
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Tissue was snap-frozen adn transferred in -70C. RNAse f
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/db_xref="taxon:10116"
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Search completed: September 2, 2005, 02:08:04 Job time : 5847 secs

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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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US-09-0715-858-1
US-09-0715-858-1
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US-09-149-727-7
US-08-819-866-1
US-09-270-957-27
US-08-630-820-5
US-08-630-820-5
US-08-630-820-5
US-09-893-525-36
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GTTGTTGAGAACAGATTG 360	CTTCCCTTCGAAGTAGAT 300	CTTCCCTTCGAAGTAGAT 300	AACACGGACTGCGAGGTC 240	CCTTCACCTACAAAACCACCTTCTACGTTCCGAAG 180 	AGCTGGAATGAGCAGTAC 120	TTGAATGGAGTTTGGAAT 60	ength 1689; Indels 0; Gaps 0;	Sequence 1, Appli Sequence 5, Appli Sequence 5, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 26, Appli Sequence 26, Appli Sequence 27, Appli Sequence 27, Appli	

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                                                                         TACGGCTGGTACATCTATCAGGGAAGGATAGAAGGAGGACTTCAAGCTCTGGAAAAAGAC 1380
                                                                                                                                                GACGAGAGAACAAGAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTAC
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APPLICANT: Podsakoff, Gregory

APPLICANT: Podsakoff, Gordon

APPLICANT: Watson, Gordon

APPLICANT: Couto, Linda B.

APPLICANT: Yang, Bin

TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS FOR TITLE OF INVENTION: TREATMENT OF LYSOSOMAL DISORDERS

FILE REFERENCE: 0800-0021

CURRENT APPLICATION NUMBER: US/09/715,858

CURRENT APPLICATION NUMBER: US/09/715,858

CURRENT FILING DATE: 2000-11-14

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin Ver. 2.0

LENGTHAL 1666
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Best Local Similarity
Matches 492; Conserv
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ORGANISM: Homo
FEATURE:
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CGCTGCCGCAGTTCTTCAACAACGTTTCTCTGCATCACCACATGCAGGTGATGGAAGAAG
                                 CAAGGTACCA---CTACAATCCCGAGACTCAGAAGATAGCAGAAGACAACATAAGAAGAA 1093
                                                                         TGCAGATGTGTGACCGCTATGGGATTGTGGTCATCGATGAGTGTCCCGGCGTGGGCCTGG
                                                                                                            TGGATCTTGCCGACAGACTCGGAATCCTTGTGATAGACGAAGCCCCGCACGTTGGTATCA 1036
                                                                                                                                                   TTCGCTGGCTTGGTGCCAACGCTTTCCGTACCAGCCACTACCCCTATGCAGAGGAAGTGA 1177
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                                                                                STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/039,555B
FILING DATE: 16-MAR-1998
                                                                                                                                                                                                                                                                                                                              APPLICANT: Koerner, Kathrin
APPLICANT: Mueller, Rolf
APPLICANT: Sadlacek, Hans-Harald
TITLE OF INVENTION: PREMARATION AND US
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMBER: DE 19710643.9
FILING DATE: 14-MAR-1997
 ATTORNEY/AGENT
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3000 K Street, N.W.,
 INFORMATION:
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INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 2191 base pairs
TYPE: nucleic acid
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REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 0167
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5390
TELEFAX: (202)672-5399
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TOPOLOGY: lin
MOLECULE TYPE:
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ACGATCAGGCTCCTTTTGAAAAA-----AGACTACATCATCGGAACACACGTGTGGGCCT 156
                                                            TCCACTACGATCCACCTCAAATGTTCTCCGAAGAGTACCAAGCAGAGCTCGTTGAAAAAG- 1512
                                                                                                                                                                                                           TCTATCAGGGAAGGATAGAAGAAGGACTTCAAGCTCTGGAAAAAGACATAGAAGAGCTCT
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                                  TTCACCAGGATCCACCTCTGATGTTCACTGAAGAGTACCAGAAAAGTCTGCTAGAGCAGT
                                                                                                        ĂTAAGAAGTATCAGAAGCCCATTATTCAGAGCGAGTATGGAGCAGAAACGATTGCAGGGT
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                                                                                                                                                                            CAGACAAGGGGGCTCCGTATGTGGATGTGATCTGTTTGAACAGCTACTACTCTTGGTATC
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Pred. No. 5.9e-43;
0; Mismatches 431;
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Best Local S
Matches 477
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APPLICANT: Couto, Linda B.
APPLICANT: Yang, Bin
APPLICANT: Yang, Bin
TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS FOR THE
TITLE OF INVENTION: TREATMENT OF LYSOSOMAL DISORDERS
FILE REFERENCE: 0800-0021
CURRENT APPLICATION NUMBER: US/09/715,858
CURRENT FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 1947
TYPE: DNA
CORDANIAM: Min TREATMENT
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                                                                                                                                                                            ACAAGGTACCACTACAATCCCGAGACTCAGAAGATAGCAGAAGACAACATAAGAAGAATG
                                                                                                                                                                                                                                              GATCTTGCCGACAGACTCGGAATCCTTGTGATAGACGAAGCCCCGCACGTTGG---TATC 1035
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TCTGCTCTGAAACCCCCCCCATATTACTTTAAGACGCTGATCACCCACACCAAAGCCCTG
                                 TCCAACCATCCAGACGCGGAGGGTTTCTTCAAAGCCCCTTTATGAGACTGCCAATGAAATG 1215
                                                                     GTTCGCCGGGACAAAATCACCCTGCGGTTGTGATGTGGTCTGTGGCCAATGAGCCTTCC
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Pred. No. 5.6e-39;
0; Mismatches 444;
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; ORGANISM: Bacillus
US-09-149-727-7
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US-09-149-727-7
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Best Local Similarity 45.4%;
Matches 734; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jefferson, Richard A.
APPLICANT: Klian, Andrzej
APPLICANT: Klian, Andrzej
APPLICANT: Keese, Paul Konrad
TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS.
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 190106.405
CURRENT APPLICATION NUMBER: US/09/149,727
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: US 60/058,263
EARLIER FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver.
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TGTGACGGGGAAAGTGAAATCCGGAGAGAACGAACTCAGGGTGGTTGTTGAGAACAGATT 359
                                                                    CTTCCTCAACGGAGAAAAGTGGGGAGAGAATCACATTGAATACCTTCCCCTTCGAAGTAGA 299
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                                                                                                                        CTATCTGAAGGATCAGCGTATCGTGCTCCGCCTTCGGCTCTGCAACTCACAAAGCAATTGT
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                                        CTATGTCAATGGTGAGCTGGTGGAGCACAAGGGCGGATTCCTGCCATTCGAAGCGGA
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Pred. No. 2.7e-33;
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                                                                     GGACAAAGTCGCCGAACTGA-----TTGACGTCATCGCGCTCAATCGCTATAACGGATG
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APPLICANT: RICHARD A. Jefferson and Jorge E. Mayer
TITLE OF INVENTION: MICROBIAL -GLUCURONIDASE GENES, GE
TITLE OF INVENTION: PRODUCTS, AND USES THEREOF
FILE REFERENCE: 190106.405C1
CURRENT APPLICATION NUMBER: US/09/270,957
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 112
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 27
LENGTH: 1888
TYPE: DNA
ORGANISM: Bacillus sp.
US-09-270-957-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.7%;
Best Local Similarity 45.4%;
Matches 734; Conservative
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                         TGGAAGTTTTCCACCTGCAAACTTCGACTTCCTTCCCCTACGGTGGAATCATAAGGCCTGT 479
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Pred. No. 7.7e-30;
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ACCAGGCGAACCACGTCGTGTTCGATGAGTTTGAGAACTTCGTGGGTGAGCAAGCGTGGA
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                                               TTGĄĄĄĄGĄCGĄTCAGGCTCCTTTTGĄĄĄĄĄĄGĄCTĄCĄTCATCGGĄĄCĄCACACGTGTGGG
                                                                                                                                               TAGCTGGCATCCACTACGATCCACCTCAAATGTTCTCCGAAGAGTACCAAGCAGAGCTCG
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US-08-819-866-1/c
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                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                            Matches 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/819,866
FILING DATE: 14-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 14683 base pair
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APPLICANT: BARNETT, Richard Spence
APPLICANT: MCLACHLAN, Karen Retta
TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT
TITLE OF INVENTION: SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS
TITLE OF INVENTION: RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE SAME
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESCEE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620
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CITY: Alexandria
STATE: Virginia
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
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  TCCTACCGTACCTCGCATTACCCTTACGCTGAAGAGATGCTCGACTGGGCAGATGAACAT 7109
                        TCTTTCAGGACCTCTCACTATCCTTACAGTGAAGAGTGGCTGGATCTTGCCGACAGACTC
                                                                          GGATTCGATAACGTGCTGATGGTGCACGACCACGCATTAATGGACTGGATTAGGGCCCAAC
                                                                                                              GGCACCTTTTATCCATTGATGATAAAAGACTTCAACCTTCTGAAGTGGATCAACGCGAAT 936
                                                                                                                                                                                                                                 TACCCGCTTCGCGTCGGCATCCGGTCAGTGGCAGTGAAGGGCGAACAGTTCCTGATTAAC
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                                                                                                                                                                                                                                                                                                                              Score 112; DB 2;
Pred. No. 1.6e-23;
                                                                                                                                                                                                                                                                                                            Mismatches 450;
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RESULT 8
US-09-023-715-1/c
                        APPLICANT: REFF, Mitchell E.
APPLICANT: BARNETT, Richard Spence
APPLICANT: BARNETT, Richard Spence
APPLICANT: BARNETT, Richard Spence
APPLICANT: MCLACHLAN, Karen Retta
TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT
TITLE OF INVENTION: SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS
TITLE OF INVENTION: RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE SAME
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. BOX 1404
CITY: Alexandria
COUNTRY: United States
TIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application Patent No. 5998144 GENERAL INFORMATION:
       COMPUTER READABLE
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       FORM:
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 14683 base pairs
TYPE: nucleic acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,71:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Teskin, Robin L.
REGIZION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 14-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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                                                                            AATGTAATGTTCTGCGACGCTCACACCGATACCATCAGCGATCT-----
                                                                                                                       AGCATGATGGACGCACCAGACGAGAGAACAAGAGACGTGGCGCTGAAGTACTTCGACATC
                                                                                                                                                                      TTCGCGCCACTGGCGGAAGCAACGCGTAAACTCGACCCGACGCGTCCGATCACCTGCGTC
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Pred. No. 1.6e-23;
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GENERAL INFORMATION:

APPLICANT: REFF, MITCHELL R.

APPLICANT: BARNETT, RICHARD S.

APPLICANT: MCLACHLAN, KAREN R.

ITILE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN TITLE OF INVENTION: WESTOR FOR ACCOMPLISHING THE SAME

ITILE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME

ITILE OF INVENTION UMBER: US/09

CURRENT APPLICATION NUMBER: US/09/343,485A

CURRENT FILING DATE: 1999-06-30

PRIOR APPLICATION NUMBER: 09/023,715

PRIOR APPLICATION NUMBER: 09/023,715

PRIOR APPLICATION NUMBER: 09/03,715

PRIOR APPLICATION NUMBER: 09/03,715

PRIOR APPLICATION NUMBER: 09/03,715

PRIOR APPLICATION NUMBER: 09/03,715

PRIOR FILING DATE: 1999-03-14

NUMBER: OF SEQ ID NOS: 3

NUMBER OF SEQ ID NOS: 3
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US-09-343-485A-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1
LENGTH: 14683
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                              Best Local Sim Matches 472;
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description OTHER INFORMATION: referred to
                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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 TCTTTCAGGACCTCTCACTATCCTTACAGTGAAGAGTGGCTGGATCTTGCCGACAGACTC
                                     GGATTCGATAACGTGCTGATGGTGCACGACCACGCATTAATGGACTGGATTAGGGCCAAC
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                                                                                                                                                                                                                       Sequence 18, Application Patent No. 5861277 GENERAL INFORMATION:
                                                                                        TITLE OF INVESTIGATION OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ARNOLD, WHITE
                                                                                                                 APPLICANT: Rose, Alan B.
APPLICANT: Last, Robert L.
APPLICANT: Last, Robert L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING TITLE OF INVENTION: THE EXPRESSION OF GENES IN PLANTS NUMBER OF SEQUENCES: 21
                               CITY: Houston
STATE: TX
                                                      ADDRESSEE: AKNOLL.
ADDRESSEE: P.O. BOX 4433
COUNTRY: UZIP: 77210
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Best Local Similarity 47.4%;
Matches 465; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPAX: 512/4/4-19: 18: INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS: SEQUENCE 13035 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: BT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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STRANDEDNESS: single
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CLASSIFICATION:
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CAAGCTCTGGAAAAGACATAGAAGAGCTCTATGCAAGGCACAGAAAGCCCATCTTTGTC 1422
                                                                                                                                                                                                                                                                                                        GTGATCATGTGGAGTGTGGCGAACGAACCAGGGTCCAACCATCCAGACGCGGAGGGTTTC 1182
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                                                                           GTCTGTGTGAACAGGTACTACGGCTGGTACATCTATCAGGGAAGGATAGAAGAAGGACTT
                                                                                                               AATGTAATGTTCTGCGACGCTCACACCGATACCATCAGCGATCT-----CTTTGATGTG
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                                     CTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGCGGCGATTTGGAAACCGCAGAG 2669
                                                                                                                                                     AGCATGATGGACGCACCAGACGAGAGAACAAGAGACGTGCGCGCTGAAGTACTTCGACATC 1302
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Pred. No. 1.4e-23;
0; Mismatches 457;
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RESULT 11
US-08-630-820-5
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Patent No. 600802
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                               TOPOLOGIA
MOLECULE TYPE: CDN
HYPOTHETICAL: NO
                                                                                                                                                                             TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195
FILING DATE: 11-APR-1995
ATTORNEY/AGENT INFORMATION:
              ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OPPER, Martin
APPLICANT: BOSSLET, Klaus
APPLICANT: CZECH, Klaus
APPLICANT: CZECH, Joerg
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
TITLE OF INVENTION: IN E. COLI
                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: (202)672-5300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                 NAME: GRANADOS, Patricia D. REGISTRATION NUMBER: 33,683 REFERENCE DOCKET NUMBER: 18
                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                            LENGTH: 3169 base pairs
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Enterobacteriaceae: Escherichia coli
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Best Local Similarity
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IMMEDIATE SOURCE:
CLONE: pTrc99 dic
FEATURE:
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ATCATCGGAACACACGTGTGGGCCTTTGCAGATTTTAAGACTCCTCAGAATGTGAGAAGA 1602
                                                                                       GAAGAGTACCAAGCAGAGCTCGTTGAAAAGACGATCAGGCTCCTTTTGAAAAAAAGACTAC 1542
                                                                                                                                                          ACAGAATTCGGTGCGGACGCGATAGCTGGCATCCACTACGATCCACCTCAAATGTTCTCC 1482
                                                                                                                                                                                            AAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAAACTGCATCAGCCGATTATCATC
                                                                                                                                                                                                                               CAAGCTCTGGAAAAAGACATAGAAGAGCTCTATGCAAGGCACAGAAAGCCCCATCTTTGTC
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                                                     GAAGAGTATCAGTGTGCATGGCTGGATATGTATCACCGCGTCTTTGATCGCGTCAGCGCC
                                                                                                                                                                                                                                                                  CTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGCGGCGATTTGGAAACGGCAGAG
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                                                                                                                           ACCGAATACGGCGTGGATACGTTAGCCGGGCTGCACTCAATGTACACCGACATGTGGAGT
                                                                                                                                                                                                                                                                                                                                                                  AGCATGATGGACGCACCAGACGAGAGAGACAAGAGACGTGGCGCTGAAGTACTTCGACATC
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; SEQUENCE DESCRIPTION: US-09-273-453-5
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US-09-273-453-5
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                                                                                                                                                                                                                                                                                                                                                                       TELEX: 904136
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION NUMBER: US/09/273,453
FILING DATE: 22-Mar-199
PRIOR APPLICATION NUMBER: 08/630,820
FILING DATE: CUNKNOWN
APPLICATION NUMBER: 08/630,820
FILING DATE: UNKNOWN
APPLICATION NUMBER: 33,683
REGISTRATION NUMBER: 33,683
REGISTRATION NUMBER: 13,683
REGISTRATION INFORMATION:
TELEPRENCE/DOCKET NUMBER: 13748/306
TELECOMMUNICATION INFORMATION:
TELEPRENCE/DOCKET NUMBER: 13748/306
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BOSSLET, Klaus
CZECH, Joerg
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODY FRAGMENT FUSION MOLECULES
ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
IN E. COLI
                                                                                                                                                                                                                                                       TOPOLOGY: circular MOLECULE TYPE: cDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: OPPER, Martin
BOSSLET, Klaus
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                                                                         FEATURE:
                                                                                                                               FEATURE:
                                                                                                                                                                    IMMEDIATE SOURCE:
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ORGANISM: Enterobacteriaceae:
                                                                                                                                                                                                                                          ANTI-SENSE: NO
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COUNTRY: USA
                                  NAME/KEY: CDS
LOCATION: 666..3162
                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                          LOCATION:
                                                                                                                                               CLONE: pTrc99 dicistr.
                                                                                                                                                                                     STRAIN: pRAJ210
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                                                                                                              NAME/KEY:
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Query Match

6.6%;

Score 110.8;

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Length 3169;

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Best Local Similarity Matches 465; Conserv
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                                                         GTACTGAGAAGACTGTGGAGTG 1684
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                                                                                            GTTGGCGGTAACAAGAAAGGGATCTTCACTCGCGACCGCAAACCGAAGTCGGCGGCTTTT 3098
                                                                                                                                ACAGAATTCGGTGCGGACGCGATAGCTGGCATCCACTACGATCCACCTCAAATGTTCTCC
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                     CTGCTGCAAAAACGCTGGACTG
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0; Mismatches 457;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Rose, Alan B.
APPLICANT: Last, Robert L.
APPLICANT: Last, Robert L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING TITLE OF INVENTION: THE EXPRESSION OF GENES IN PLANTS NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19, Application Patent No. 5861277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKST NUMBER: BT:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/723,624 FILING DATE: Concurrently Herewit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 77210
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CITY: Houston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: ARNOLD, WHITE & DURKEE STREET: P.O. Box 4433
    1123
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GTGATCATGTGGAGTGTGGCGAACGAACCAGAGTCCAACCATCCAGACGCGGAGGGTTTC 1182
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                                                CAGCAAGCGCACTTACAGGCGATTAAAGAGCTGATAGCGCGTGACAAAAACCACCCAAGC
                                                                                            TTCGAAGCGGGCAACAAGCCGAAAGAACTGTACAGCGAAGAGGCAGTCAACGGGGAAACT
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Pred. No. 1.7e-23;
0; Mismatches 457;
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CURRENT APPLICATION NUMBER: US/09/893,525
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 09/210,843
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: US 08/846,021
PRIOR APPLICATION NUMBER: US 08/846,021
PRIOR APPLICATION NUMBER: US 08/366,783
PRIOR FILING DATE: 1994-12-30
PRIOR FILING DATE: 1994-12-30
PRIOR FILING DATE: 1993-11-16
PRIOR APPLICATION NUMBER: US 08/142,418
PRIOR APPLICATION NUMBER: US 07/659,835
PRIOR APPLICATION NUMBER: US 07/659,835
PRIOR FILING DATE: 1991-02-22
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PATENTIN ONS: 42
SOFTW
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US-09-893-525-36
; Sequence 36, Application
; Patent No. 6753167
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LOCATION: (1548)..(3359)
OTHER INFORMATION:
-09-893-525-36
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APPLICANT: Van Rooijen, Gijs
TITLE OF INVENTION: Preparation of Heterologous Proteins on Oil Bodies
FILE REFERENCE: 9369-172
                                                                  ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Phas-GUS-phas
NAME/KEY: CDS
                                                                                                                                                                         TYPE: DNA
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Sequence 41, Application US/09893525

Sequence 11, Application US/09893525

Patent No. 6753167

GENERAL INFORMATION:

APPLICANT: Moloney, Maurice M.

APPLICANT: Wolney, Maurice M.

APPLICANT: Van Rooijen, Gije

TITLE OF INVENTION: Preparation of Heterologous Proteins on Oil Bodi

FILE REFERENCE: 9369-172

CURRENT APPLICATION NUMBER: US/09/893,525

CURRENT FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US 09/210,843

PRIOR FILING DATE: 1998-12-15

PRIOR FILING DATE: 1998-12-15

PRIOR APPLICATION NUMBER: US 08/866,783

PRIOR APPLICATION NUMBER: US 08/366,783

PRIOR FILING DATE: 1994-12-30

PRIOR APPLICATION NUMBER: US 08/366,783

PRIOR FILING DATE: 1993-11-16

PRIOR APPLICATION NUMBER: US 08/142,418

PRIOR FILING DATE: 1993-11-16

PRIOR APPLICATION NUMBER: US 07/659,835

PRIOR FILING DATE: 1991-02-22

VNTABED OF CEO IN NOS. 42
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; NAME/KEY: CDS
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                                                          GTGGTGATGTGGAGTATTGCCAACGAACCGGATACCCGTCCGCAAGGTGCACGGGAATAT
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Search completed: September 1, 2005, 19:13:25
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US-10-272-531A-5

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Sequence 14, Appl
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16, App 33, App 105, Ap 105, Ap 31, App 21, App 22, Appl 22, Appl 43, Appl 41, Appl 49, Appl	109	Sequence 343, App Sequence 16, Appl Sequence 7, Appl Sequence 215, Appl Sequence 31, Appl Sequence 3, Appl Sequence 3, Appl Sequence 45, Appl Sequence 45, Appl Sequence 5, Appl Sequence 7, Appl Sequence 27, Appl Sequence 2108, Appl Sequence 108, App

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RESULT 1

US-10-364-649-14
; Sequence 14, Application US/10364649
; Publication No. US20030229921A1
; Publication No. MICROBIAL B-GLUCURONIDASE GENES, GENE
; TITLE OF INVENTION: MICROBIAL B-GLUCURONIDASE GENES, GENE
; TITLE OF INVENTION: MICROBIAL B-GLUCURONIDASE GENES, GENE
; TITLE OF INVENTION: NUMBER: US/10/364,649
; TITLE OF INVENTION NUMBER: US/10/364,649
; PRIOR APPLICATION NUMBER: US/9/270,957
; PRIOR FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: US 09/270,957
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 112
; PRIOR APPLICATION NUMBER: US 09/270,957
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 112
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; SEQ ID NO 14
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Query Match Best Local Similarity Matches 1688; Conserv

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GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Slater, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (5205.2)
FILE REFERENCE: 38-10 (5205.2)
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/360,039
PRIOR APPLICATION NUMBER: US/03-02-28
PRIOR APPLICATION NUMBER: US/0360,039
PRIOR FILING DATE: 2002-02-21
VOLUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 26682
; LENGTH: 1692
; TYPE: DNA
; ORGANISM: Thermotoga m
; ORGANISM: 76682
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Sequence 1, Application US/10757093
; Publication No. US20050153448A1
; GENERAL INFORMATION:
; APPLICANT: CAMBIA
; TITLE OF INVENTION: Fungal beta-glucuronidase gen
; FILE REFERENCE: 415
; CURRENT APPLICATION NUMBER: US/10/757,093
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Scopulariopsis sp. isoate RP38.3
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CURRENT FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: US 60/287,531
PRIOR FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: US 60/304,609
PRIOR APPLICATION NUMBER: US 60/329,461
PRIOR PRIOR PILING DATE: 2001-10-15
PRIOR RETLING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/351,276
PRIOR APPLICATION NUMBER: US 60/351,276
PRIOR PILING DATE: 2002-01-23
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 5
LENGTH: 2169
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                Matches
                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LeBowitz, Jonathan
APPLICANT: Beverley, Stephen
TITLE OF INVENTION: SUBCELLULAR TARGETING
FILE REFERENCE: SYM-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/136,841
CURRENT FILING DATE: 2002-08-22
                                                                                                                                                                                                                                                                                       OTHER INFORMATION: A recombinant sequence incorporating a signal peptide sequence, OTHER INFORMATION: the mature human beta-glucuronidase sequence, a bridge of three OTHER INFORMATION: amino acids, and an IGF-II sequence FEATURE:
                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: (1)..(2166)
                                                                                                                                                                 Local Similarity
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Pred. No. 9.8e-45;
0; Mismatches 430
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                                                                                                                                                                      Sequence 5, Application US/10272531A Publication No. US20040005309A1 GENERAL INFORMATION:
FILE REFERENCE: SYM-009
CURRENT APPLICATION NUMBER: US/10/272,531A
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: US 60/384,452
PRIOR FILING DATE: 2002-05-29
                                                                                          APPLICANT: LeBowitz, Jonathan H
APPLICANT: Beverley, Stephen
APPLICANT: By William S.
TITLE OF INVENTION: TARGETED THERAPEUTIC PROTEINS
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PRIOR FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: US 60/408,816
PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 22
; SOPTWARE: Patentin version 3.1
; SEQ ID NO 5
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Best Local Similarity 52.2%;
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LOCATION: (1)..(2166)
OTHER INFORMATION:
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 TCCACTACGATCCACCTCAAATGTTCTCCGAAGAGTACCAAGCAGAGCTCGTTGAAAAAG-
                                       ATAAGAAGTATCAGAAGCCCATTATTCAGAGCGAGTATGGAGCAGAAACGATTGCAGGGT 1648
                                                                                                              ACGACTACGGGCACCTGGAGTTGATTCAGCTGCAGCTGGCCACCCAGTTTGAGAACTGGT
                                                                                                                                                  TCTATCAGGGAAGGATAGAAGAAGACTTCAAGCTCTGGAAAAAGACATAGAAGAGCTCT
                                                                                                                                                                                                                             GAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTACTACGGCTGGTACA 1333
                                                                                                                                                                                                                                                                                                                                            CGTCCCACCTAGAATCTGCTGGCTACTACTTGAAGATGGTGATCGCTCACACCAAATCCT
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                                                                         ATGCAAGGCACAGAAAGCCCATCTTTGTCACAGAATTCGGTGCGGACGCGATAGCTGGCA
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Pred. No. 9.8e-45;
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US-10-272-483A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NUMBER OF SEQ ID NOS: 22; SOFTWARE: PatentIn version; SEQ ID NO 5; LENGTH: 2169
; TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/10272483A Publication No. US20040006008A1
                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                      Matches 493;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: SYM-007CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Beverley, Stephen
TITLE OF INVENTION: TARGETED THERAPEUTIC PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LeBowitz, Jonathan H
                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: A recombinant DNA sequence incorporating a signal peptide sequenc OTHER INFORMATION: e, the mature human beta-glucuronidase sequence, a bridge of thre OTHER INFORMATION: e amino acids, and an IGF-II sequence
                                                                                                                                                                                                                                                                                                                    LOCATION: (1)..(2166)
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
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APPLICATION NUMBER: US 60/408,816
FILING DATE: 2002-09-06
APPLICATION NUMBER: US 60/304,609
FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 10/136,841
FILING DATE: 2002-04-30
APPLICATION NUMBER: US 60/384,452
FILING DATE: 2002-05-29
APPLICATION NUMBER: US 60/386,019
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AATTCCCCGTTCTGGGGCAGGGCACCTTTTATCCATGATGATAAAAGACTTCAACCTTC
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                                                           AGAGCCAGTTCCTCATCAATGGGAAACCTTTCTATTTCCACGGTGTCAACAAGCATGAGG
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Pred. No. 9.8e-45;
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                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Podsakoff, Gregory
APPLICANT: Watson, Gordon
                                                                                                                                                                                                                                                                           Sequence 1, Application US/10421175 Publication No. US20030219414A1
              TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS TITLE OF INVENTION: TREATMENT OF LYSOSOMAL DISORDERS FILE REFERENCE: 0800-0021 CURRENT APPLICATION NUMBER: US/10/421,175 CURRENT FILING DATE: 2003-04-22 PRIOR APPLICATION NUMBER: US/9/715,858 PRIOR APPLICATION STATES OF SECULATION OF SECULATION NUMBER: US/99/715,858 PRIOR FILING DATE: 2000-11-14 NUMBER OF SECULATION NUMBER: US/99/715,858 PRIOR FILING DATE: 2000-11-14
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APPLICANT:
  SOFTWARE:
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Couto, Linda B.
Yang, Bin
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; LENGTH: 1956
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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Best Local Similarity
Matches 492; Conserv
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LOCATION: (1)..(1956)
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                      TTGCAGATTTTAAGACTCCTCAGAATGTGAGAAGACCCATTCTCAACCAAGAGGGTGTTT
                                                                                            ACGATCAGGCTCCTTTTGAAAAA-----AGACTACATCATCGGAACACACGTGTGGGCCT
                                                                                                                                                                  TCCACTACGATCCACCTCAAATGTTCTCCCGAAGAGTACCAAGCAGAGCTCGTTGAAAAG-
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TTGCCGATTTCATGACTGAACAGTCACCGACGAGAGTGCTGGGGGAATAAAAAGGGGGATCT
                                                                      ACCATCTGGGTCTGGATCAAAAACGCAGAAAATATGTGGTTGGAGAGCTCATTTGGAATT
                                                                                                                                          TTCACCAGGATCCACCTCTGATGTTCACTGAAGAGTACCAGAAAAGTCTGCTAGAGCAGT
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Sequence 343, Application US/10388360
Publication No. US20030225528A1
GENERAL INFORMATION:
APPLICANT: GENOMIC HEALTH
APPLICANT: Baker, Joffre B.
APPLICANT: Cronin, Maureen T.
APPLICANT: Kiefer, Michael C.
APPLICANT: Shak, Steve
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; ORGANISM: Homo
US-10-388-360-343
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TITLE OF INVENTION: GENE EXPRESSION PROFILING IN
FILE REFERENCE: 39740-0001US
CURRENT APPLICATION NUMBER: US/10/388,360
CURRENT FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 60/412,049
PRIOR APPLICATION NUMBER: US 60/412,049
PRIOR APPLICATION NUMBER: US 60/364,890
PRIOR APPLICATION NUMBER: US 60/364,890
PRIOR FILING DATE: 2002-03-13
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US-10-388-360-343
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Best Local S
Matches 492
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 343
LENGTH: 2191
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GAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTACTACGGCTGGTACA 1333
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                                    TGGACCCCTCCCGGCCTGTGACCTTTGTGAGCAACTCTAACTATGCAG--
                                                                     TGGATCGAACACGCCCCTTGTCATGGTGAGCATGATGGACGCACCAGACGAGAGAACAA
                                                                                                              CGTCCCACCTAGAATCTGCTGGCTACTACTTGAAGATGGTGATCGCTCACACCAAATCCT
                                                                                                                                             AGTCCAACCATCCAGACGCGGAGGGTTTCTTCAAAGCCCCTTTATGAGACTGCCAATGAAA 1213
                                                                                                                                                                                                                                                             CGCTGCCGCAGTTCTTCAACAACGTTTCTCTGCATCACCACGATGCAGGTGATGGAAGAAG
                                                                                                                                                                                                                                                                                                CAAGGTACCA---CTACAATCCCGAGACTCAGAAGATAGCAGAAGACAACATAAGAAGAA
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nilarity 52.1%;
Conservative
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Pred. No. 3.3e-44;
0; Mismatches 431;
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PRIOR APPLICATION NUMBER: 60/377,672
PRIOR FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 16
LENGTH: 2191
TYPE: DNA
ORGANISM: Homo sapiens
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US-10-429-802-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/10429802
Publication No. US20030228285A1
GENERAL INFORMATION:
APPLICANT: HUNG, MIEN-CHIE
APPLICANT: WONG, KA YIN
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                              Matches 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: BIPARTITE T-CELL FACT
FILE REFERENCE: UTSC:752US
CURRENT APPLICATION NUMBER: US/10/429,802
CURRENT FILING DATE: 2003-05-05
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ZOU, YIYU
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                                                                                                                                                                                                                                                                                         10.2%;
                                                                                                                                                                                                                                                                              0; Mismatches 431;
                                                                                                                                                                                                                                                                                           Score 172.4; DB 1
Pred. No. 3.3e-44;
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Query Match
Best Local Similarity
                                                   TYPE: DNA
ORGANISM: Homo
                                                                               LENGTH: 2191
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US-10-430-503-7
; Sequence 7, Application US/10430503
; Publication No. US20040005684A1
; GENERAL INFORMATION:
CURRENT APPLICATION NUMBER: US/10/430,503
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 60/383,063
PRIOR FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HUNG, MIEN-CHIE
APPLICANT: LAN, KENG-LI
APPLICANT: OU-YANG, FU
APPLICANT: LIU, JAW-CHING
APPLICANT: LAN, KENG-HSIN
                                                                                                                                                                                                                                                 TITLE OF INVENTION: TARGETING TITLE OF INVENTION: REAGENTS FILE REFERENCE: UTSC:797US
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Score 172.4; DB 1 Pred. No. 3.3e-44;

DB 17;

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RESULT 11
US-10-335-053-51
; Sequence 51, Application US/103:
; Publication No. US20040241653A1
; GENERAL INFORMATION:
; APPLICANT: Quark Biotech, Inc.
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Best Local Sim
Matches 492;
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CURRENT APPLICATION NUMBER: 0703-070/US3 CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: 60/345,317
PRIOR FILING DATE: 2001-12-31
NUMBER OF SEQ ID NOS: 319
SOFTWARE: PATENTIN Version 3.2
SEQ ID NO 51
LENGTH: 2191
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                              ACGATCAGGCTCCTTTTGAAAAA-----AGACTACATCATCGGAACACACGTGTGGGCCT
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                                                                   TTCACCAGGATCCACCTCTGATGTTCACTGAAGAGTACCAGAAAAGTCTGCTAGAGCAGT
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Pred. No. 3.3e-44;
0; Mismatches 431;
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CUERENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 0205336.9
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 862
SOFTWARE: Patentin version 3.1
SEQ ID NO 225
LENGTH: 2472
TYPE: DNA
ORGANISM: Rattus norvegicus (No. US20040005547Alway rat)
US-10-388-934-225
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Best Local Similarity 51.3%;
Matches 477; Conservative (
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Best Local Similarity
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APPLICANT: Wolf, Detlef
TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
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                             CCCGTTGTCATGGTGAGCATGATGGACGCACCAGACGAGAGAACAAGAGAGACGTGGCGCTG
                                                                             CCTGCCGGATATTACTTCAAGACGCTGATCGCCCACACCAAAGCCCCTGGACCCCACCCGT
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-- CCAGATATGACGCAGACATGGGGGCC
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US-10-421-175-3
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; LENGTH: 1947
; TYPE: DNA
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Best Local Similarity 50.6%;
Matches 477; Conservative
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Publication No. US20030219414A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Watson, Gordon
APPLICANT: Couto, Linda B.
APPLICANT: Couto, Linda B.
APPLICANT: Yang, Bin
TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS |
TITLE OF INVENTION: TREATMENT OF LYSOSOMAL DISORDERS
FILE REPERENCE: 0800-0021
CURRENT APPLICATION NUMBER: US/10/421,175
CURRENT FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: US/09/715,858
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Podsakoff, Gregory
APPLICANT: Watson, Gordon
APPLICANT: Couto, Linda B.
APPLICANT: Yang, Bin
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                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1947)
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                                                                                                                                                                                                   GAACTTGAAAAAGACGAGTACACTCTGGACATCGGAATCAGAACGATCAGCTGGGACGAG
TCAGATATCCGAGGGAAAGGCTTCGACTGGCCGCTGCTGGTAAAGGATTTCAACCTGCTC
                                                                                                                   AAGAGGCTCTATCTGAACGGGAAACCTGTCTTTTTGAAGGGCTTTGGAAAGCACGAGGAA
                                                                                                                                                               GAGTCTGTGACTACTACACCCTTCCTATCGGGATTCGAACAGTGGCTGTCACAAAG
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                                   TTCCCCGTTCTGGGGCAGGGCACCTTTTATCCATTGATGATAAAAGACTTCAACCTTCTG
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Pred. No. 4.4e-40;
0; Mismatches 444; Indels 21;
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Sequence 3, Application US/10757093
Publication No. US20050153448A1
GENERAL INFORMATION:
APPLICANT: CAMBIA
TITLE OF INVENTION: Fungal beta-glucuronidase geielle Reference: 415
CURRENT APPLICATION NUMBER: US/10/757,093
CURRENT FILING DATE: 2004-01-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.2
SEQ ID NO 3
                                                                             ; TYPE: DNA
; ORGANISM: Penicillium
US-10-757-093-3
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US-10-757-093-3
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  Score 141.6; DB Pred. No. 3e-34;
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APPLICANT: JEFFERSON, Richard A.
APPLICANT: Kilian, Andrzej
APPLICANT: Kilian, Andrzej
APPLICANT: Keese, Paul Konrad
TITLE CANT: Keese, Paul Konrad
TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 19016.405
CURRENT FERFERENCE: 19016.405
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/149,727
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/149,727
PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US 60/058,263
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
SEQ ID NO 7
LENGTH: 1887
TYPE: DNA
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Publication No. US20030157684A1
GENERAL INFORMATION:
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ORGANISM: Bacillus
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Search completed: September 1, 2005, 21:26:50 Job time : 1170 secs